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ME

STIC-Biotech/ChemLib

From: Slobodyansky, Elizabeth
Sent: Tuesday, August 22, 2006 6:23 PM
To: STIC-Biotech/ChemLib
Subject: 10665715 seq

STIC

10665715

Please search for case 10/665,715:

28

SEQ ID NO: 16 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner
Art Unit 1652
REM 2D83
571-272-0941
MAILBOX 2C70

10-665-715

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 8-25-06
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:13:17 ; Search time 194 Seconds
(without alignments)
1277.378 Million cell updates/sec

Title: US-10-665-715-16

Perfect score: 2879

Sequence: 1 MEPDSVIDKTIELMCSVPR.....PPSAQNRTSPSTVTYISR 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*
- 10: geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2879	100.0	542	3	Aay96696 Human E3
2	2879	100.0	542	4	Aam79127 Human pro
3	2879	100.0	542	4	Aam40208 Human pol
4	2879	100.0	542	8	AdS88293 Human pro
5	2879	100.0	542	9	Aea01728 Human bet
6	2879	100.0	550	4	Aam41994 Human pol
7	2873	99.8	542	9	AdX05377 Cyclin-de
8	2755.5	95.7	563	8	AdS88282 Human pro
9	2666.5	92.6	529	9	AdX05979 Cyclin-de
10	2661	92.4	508	9	AdX05981 Cyclin-de
11	2458.5	85.4	579	4	Aam78583 Human pro
12	2445.5	84.9	605	4	Aam78582 Human pro
13	2445.5	84.9	605	8	AdS88274 Human pro
14	2423	84.2	654	4	Aam79568 Human pro
15	2423	84.2	654	4	Aam79567 Human pro
16	2423	84.2	654	4	Aam79566 Human pro
17	2422	84.1	632	4	Aam78584 Human pro
18	2421	84.1	590	4	Aam00847 Human bon
19	2385.5	82.9	608	4	Aam00960 Human bon
20	2384.5	82.8	569	2	Aay24054 A human b
21	2384.5	82.8	569	3	Aay44249 Human cel
22	2384.5	82.8	569	3	Aab12813 Human bet
23	2384.5	82.8	569	3	Aay96697 Human bet

24	2384.5	82.8	569	3	AAY83250	F-box pro
25	2384.5	82.8	569	3	AAY83041	F-box pro
26	2384.5	82.8	569	5	ABG69473	Human bai
27	2384.5	82.8	569	5	AAO22446	Human F-b
28	2384.5	82.8	569	8	ADS88273	Human pro
29	2384.5	82.8	569	9	ADY62359	Human F-b
30	2384.5	82.8	569	9	AEA01725	Human bet
31	2377.5	82.6	569	4	AAAB48298	Human 2F1
32	2375.5	82.5	569	3	AAAB12812	Mouse ubi
33	2375.5	82.5	569	3	AAY83254	F-box pro
34	2375.5	82.5	1443	9	AEC34365	Mutant be
35	2286.5	79.4	517	2	AAAR85852	WD-40 dom
36	2077.5	72.2	510	4	ABBS9857	Drosophil
37	1638.5	56.9	701	8	ADN22767	Bacterial
38	1143	39.7	265	4	AAU86942	Human DNA
39	816	28.3	159	4	ADM20097	Protein e
40	723.5	25.1	204	8	ADP29897	Human sec
41	693.5	24.1	219	5	AAU98087	Human bet
42	675.5	23.5	158	4	ADM19852	Protein e
43	664	23.1	131	4	ADM19861	Protein e
44	654	22.7	1326	4	ABB67237	Drosophil
45	654	22.7	1326	4	ABB70051	Drosophil

ALIGNMENTS

RESULT 1

AAI96696
ID AAY96696 standard; protein; 542 AA.

AC AAY96696;

DT 26-SEP-2000 (first entry)

DE Human E3 ubiquitin ligase.

XX E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KW anti-inflammatory; immunosuppressive; cytostatic.

OS Homo sapiens.

PN WO200034447-A2.

PD 15-JUN-2000.

PF 09-DEC-1999; 99WO-US029371.

PR 10-DEC-1998; 98US-00210060.

XX (SIGN-) SIGNAL PHARM INC.
XX (YISS) YISSUM RES & DEV CO.

PI Manning AM, Mercurio F, Amit S, Ben-Neriah Y, Davis M;
PI Hatzubai A; Lavon I, Yaron A;

DR WPI; 2000-431294/37.
DR N-PSDB; AAA51228.

XX Polypeptide enhancing phosphorylated IkkappaB ubiquitination useful for
PT treating disorder associated with NF-kappaB activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
variant.

XX Claim 1; Page 70-72; 77pp; English.

CC This is human E3 ubiquitin ligase (E3), which is homologous to human beta
CC -TrCP, an F-box/WD protein family member. E3 enhances ubiquitination of
CC phosphorylated I-kappa-B, an inhibitor protein of nuclear factor kappa-B
CC (NF-kappa-B). Understanding I-kappa-B degradation via the ubiquitin
CC pathway is useful for identifying modulators of this process for use in
CC treating diseases associated with activation of NF-kappa-B. In vitro

CC analysis suggests that deletion of the F-box results in a protein that
CC functions as a dominant negative molecule in vivo. Transient over-
CC expression of delta-beta-TrCP (a deletion mutant) inhibited the
CC degradation of endogenous I-kappa-B-alpha in stimulated Jurkat cells,
CC resulting in accumulation of phosphorylated I-kappa-B-alpha. E3 can be
CC used to screen for modulators of NF-kappa-B activity. E3 and beta-TrCP
CC can be used to modulate NF-kappa-B to treat inflammatory diseases,
CC autoimmune diseases, cancer and viral infections
XX
SQ Sequence 542 AA;

Query Match 100.0%; Score 2879; DB 3; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.8e-265;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLQISNGTSSVIVS 60
Db |||||
Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLQISNGTSSVIVS 60
Db |||||
Qy 61 RKRPSGNYQKEKDLCKIKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYLKPKMLQDFI 120
Db |||||
Qy 61 RKRPSGNYQKEKDLCKIKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYLKPKMLQDFI 120
Db |||||
Qy 121 TALPEQGLDHIAENILSYLDARSLCAAEVCKEQRVISEGMLWKKLIERMVTRDPLWKG 180
Db |||||
Qy 121 TALPEQGLDHIAENILSYLDARSLCAAEVCKEQRVISEGMLWKKLIERMVTRDPLWKG 180
Db |||||
Qy 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRHNLQIQRSSENS 240
Db |||||
Qy 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRHNLQIQRSSENS 240
Db |||||
Qy 241 KGVYCLQYDDEKIISGLRDNISIKIWDKTSLECLKVLTKGHTGVSVCLOYDERVIVTGSSDS 300
Db |||||
Qy 241 KGVYCLQYDDEKIISGLRDNISIKIWDKTSLECLKVLTKGHTGVSVCLOYDERVIVTGSSDS 300
Db |||||
Qy 301 TVRVWDVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
Db |||||
Qy 301 TVRVWDVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
Db |||||
Qy 361 GHRAAVNVDPDDKYIIVSAGSDRTIKVWSTSTCFVRTLNGHKGACIACQYRDLRVVSGS 420
Db |||||
Qy 361 GHRAAVNVDPDDKYIIVSAGSDRTIKVWSTSTCFVRTLNGHKGACIACQYRDLRVVSGS 420
Db |||||
Qy 421 SDNTIRLWDIECGACLRVLEGHEBELVRCIRPDNKRIVSGAYDGKIKVWDLOAALDPRAPA 480
Db |||||
Qy 481 STLCLRTLVEHSGRVPRQLQDFEFOIISSSHDDTLLIWDFLNVPSPAQNETRSPRTYTI 540
Db |||||
Qy 541 SR 542
Db |||||
Qy 541 SR 542
Db |||||

RESULT 2
AAM79127
ID AAM79127 standard; protein; 542 AA.
XX
AC AAM79127;
XX
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1789.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX

PN WO200157190-A2.
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US0004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejman T, Goodrich R;
XX WPI; 2001-476283/51.
DR N-PSDB; AAK52260.
DR
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
PT
XX Claim 20; Page 4147-4148; 6221pp; English.
PS
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 542 AA;

Query Match 100.0%; Score 2879; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.8e-265;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLQISNGTSSVIVS 60
Db |||||
Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLQISNGTSSVIVS 60
Db |||||
Qy 61 RKRPSGNYQKEKDLCKIKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYLKPKMLQDFI 120
Db |||||
Qy 61 RKRPSGNYQKEKDLCKIKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYLKPKMLQDFI 120
Db |||||
Qy 121 TALPEQGLDHIAENILSYLDARSLCAAEVCKEQRVISEGMLWKKLIERMVTRDPLWKG 180
Db |||||
Qy 121 TALPEQGLDHIAENILSYLDARSLCAAEVCKEQRVISEGMLWKKLIERMVTRDPLWKG 180
Db |||||
Qy 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRHNLQIQRSSENS 240
Db |||||
Qy 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRHNLQIQRSSENS 240
Db |||||
Qy 241 KGVYCLQYDDEKIISGLRDNISIKIWDKTSLECLKVLTKGHTGVSVCLOYDERVIVTGSSDS 300
Db |||||
Qy 241 KGVYCLQYDDEKIISGLRDNISIKIWDKTSLECLKVLTKGHTGVSVCLOYDERVIVTGSSDS 300
Db |||||
Qy 301 TVRVWDVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
Db |||||
Qy 301 TVRVWDVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
Db |||||

Qy 361 GHRAAVNVDFDDKYIVSASGDRITKWSSTCEPVRTLNHGKRGIAQLQYDRDLVWSGS 420
 Db 361 GHRAAVNVDFDDKYIVSASGDRITKWSSTCEPVRTLNHGKRGIAQLQYDRDLVWSGS 420
 Qy 421 SDNTIRLWDIECGACLRVLEGHLELVRCIRFDNKRIVSGAYDGKIKWDLQAALDPRAPA 480
 Db 421 SDNTIRLWDIECGACLRVLEGHLELVRCIRFDNKRIVSGAYDGKIKWDLQAALDPRAPA 480
 Qy 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILIWDFLNVPPSAQNTPSPRTYTYI 540
 Db 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILIWDFLNVPPSAQNTPSPRTYTYI 540
 Qy 541 SR 542
 Db 541 SR 542
 RESULT 3
 AAM40208
 ID AAM40208 standard; protein; 542 AA.
 AC AAM40208;
 XX
 DT 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 3353.
 DE
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-0052317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSEQ-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI59364.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 XX Example 5; SEQ ID NO 3353; 10078pp; English.
 PS
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 SQ Sequence 542 AA;
 Query Match 100.0%; Score 2879; DB 4; Length 542;
 Best Local Similarity 100.0%; Pred. No. 2.8e-265;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPVRCLOISNGTSSVIVS 60
 Db 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPVRCLOISNGTSSVIVS 60
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 Db 61 RKRPSGNYQKEDLCIKYFDOWSESQDVEFEHLISRMCHYQHGHINSYLPKMLQORDFI 120
 Qy 121 TALPEQGLDHAENILSYLDARSLCAAELVCKEQRVISEGMLWKLIERMVRTDPLWK 180
 Db 121 TALPEQGLDHAENILSYLDARSLCAAELVCKEQRVISEGMLWKLIERMVRTDPLWK 180
 Qy 181 LSERGHGDOYLFKRPDTPGPNSEYRSLYPKIIODIETIESNRCGRHNLQIOCRSENS 240
 Db 181 LSERGHGDOYLFKRPDTPGPNSEYRSLYPKIIODIETIESNRCGRHNLQIOCRSENS 240
 Qy 241 KGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTGS 300
 Db 241 KGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTGS 300
 Qy 301 TVRVMDVNTGEVLNLTLIHNEAVLHLRFSNGLMVTCSKDRSIAVMDNASATDITLRRVLV 360
 Db 301 TVRVMDVNTGEVLNLTLIHNEAVLHLRFSNGLMVTCSKDRSIAVMDNASATDITLRRVLV 360
 Qy 361 GHRAAVNVDFDDKYIVSASGDRITKWSSTCEPVRTLNHGKRGIAQLQYDRDLVWSGS 420
 Db 361 GHRAAVNVDFDDKYIVSASGDRITKWSSTCEPVRTLNHGKRGIAQLQYDRDLVWSGS 420
 Qy 421 SDNTIRLWDIECGACLRVLEGHLELVRCIRFDNKRIVSGAYDGKIKWDLQAALDPRAPA 480
 Db 421 SDNTIRLWDIECGACLRVLEGHLELVRCIRFDNKRIVSGAYDGKIKWDLQAALDPRAPA 480
 Qy 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILIWDFLNVPPSAQNTPSPRTYTYI 540
 Db 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILIWDFLNVPPSAQNTPSPRTYTYI 540
 Qy 541 SR 542
 Db 541 SR 542
 RESULT 4
 ADS88293
 ID ADS88293 standard; protein; 542 AA.
 XX
 AC ADS88293;
 XX
 XX 18-NOV-2004 (first entry)
 DT
 DE Human protein of a TNF-alpha signalling pathway protein complex Seq 148.
 XX
 KW protein complex; tumour necrosis factor-alpha signalling pathway;
 KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
 KW inflammatory bowel disease; infectious disease; septic shock;
 KW bacterial infection; neurological disease; stroke-induced inflammation;
 KW neurodegenerative disease; cancer; antinflammatory; antiarthritic;
 KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
 XX

CC short interfering RNA (siRNA) molecule. A method of reducing Cdc25A
CC degradation in a cell involves reducing beta-TrCP activity by reducing
CC the amount of beta-TrCP1 and/or TrCP2 in the cell e.g. by administering
CC an antisense or siRNA molecule. The methods, inhibitors, agents, and
CC compositions of the invention are useful for treating cancers, including
CC metastatic and primary cancers, and cancers characterized by solid or non
CC -solid tumors.

XX SQ Sequence 542 AA;

Query Match 100.0%; Score 2879; DB 9; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.9e-265;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCIQISNGTSVVVS 60
Db 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCIQISNGTSVVVS 60
Qy 61 RRPSEGNQYQEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHSINSLKPMQLORDFI 120
Db 61 RRPSEGNQYQEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHSINSLKPMQLORDFI 120
Qy 121 TALPEQGLDHTAENILSYLDARSLCAAEVLCKEQRVISEGMLWKKLIETRMVTRDPLWKG 180
Db 121 TALPEQGLDHTAENILSYLDARSLCAAEVLCKEQRVISEGMLWKKLIETRMVTRDPLWKG 180
Qy 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIODIETIESNWRGCRHNLQRIQCRSENS 240
Db 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIODIETIESNWRGCRHNLQRIQCRSENS 240
Qy 241 KGVYCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTSSSDS 300
Db 241 KGVYCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTSSSDS 300
Qy 301 TVRVWDVNTGEVNLTIHNEAVLHLRFSNGLMVTCKDRISIAVWDMASATDITLRRVLV 360
Db 301 TVRVWDVNTGEVNLTIHNEAVLHLRFSNGLMVTCKDRISIAVWDMASATDITLRRVLV 360
Qy 361 GHRAAVNVDPDDKIIVSASGDRITKWMSTSTCFVRLTNGHKGICLQYDRDLVWGS 420
Db 361 GHRAAVNVDPDDKIIVSASGDRITKWMSTSTCFVRLTNGHKGICLQYDRDLVWGS 420
Qy 421 SDNTIRLWDIECGACLRVLEHGEELVRCIRFDNKRIVSGAYDGKIKWMDLQAALDPRA 480
Db 421 SDNTIRLWDIECGACLRVLEHGEELVRCIRFDNKRIVSGAYDGKIKWMDLQAALDPRA 480
Qy 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSPSRVTYI 540
Db 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSPSRVTYI 540
Qy 541 SR 542
Db 541 SR 542

RESULT 6

AA41994

ID AA41994 standard; protein; 550 AA.

XX

AC AA41994;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 6925.

XX

KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX' Homq, sapiens.
OS

XX WO200153312-A1.
PN
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
FA
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
DR N-PSDB; AAI61150.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
as central nervous system injuries.
PS Example 2; SEQ ID NO 6925; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nontropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX SQ Sequence 550 AA;

Query Match 100.0%; Score 2879; DB 4; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.9e-265;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCIQISNGTSVVVS 60
Db 9 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCIQISNGTSVVVS 68
Qy 61 RRPSEGNQYQEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHSINSLKPMQLORDFI 120
Db 69 RRPSEGNQYQEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHSINSLKPMQLORDFI 128
Qy 121 TALPEQGLDHTAENILSYLDARSLCAAEVLCKEQRVISEGMLWKKLIETRMVTRDPLWKG 180
Db 129 TALPEQGLDHTAENILSYLDARSLCAAEVLCKEQRVISEGMLWKKLIETRMVTRDPLWKG 188
Qy 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIODIETIESNWRGCRHNLQRIQCRSENS 240
Db 189 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIODIETIESNWRGCRHNLQRIQCRSENS 248
Qy 241 KGVYCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTSSSDS 300
Db 249 KGVYCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTSSSDS 308

QY 301 TVRVWDVNTGEVLNTLIHNEAVLHFRFNSGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
 DB 309 TVRVWDVNTGEVLNTLIHNEAVLHFRFNSGLMVTCSKDRSIAVWDMASATDITLRRVLV 368
 QY 361 GHRAAVNVVDFDDKYIVSASGDRRTIKVWSTSTCEVFTLNGHKGRIACIQYRDLRVVSGS 420
 DB 369 GHRAAVNVVDFDDKYIVSASGDRRTIKVWSTSTCEVFTLNGHKGRIACIQYRDLRVVSGS 428
 QY 421 SDNTIRLWDIECGACLRVLEGGHEELVRCIRFNDKRIVSGAYDGKIIVWDLQAALDPRAPA 480
 DB 429 SDNTIRLWDIECGACLRVLEGGHEELVRCIRFNDKRIVSGAYDGKIIVWDLQAALDPRAPA 488
 QY 481 STLCRLTLVEHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSRPTTYI 540
 DB 489 STLCRLTLVEHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSRPTTYI 548
 QY 541 SR 542
 DB 549 SR 550

RESULT 7
 ADX05977
 ID ADX05977 standard; protein; 542 AA.
 AC ADX05977;
 DT 21-APR-2005 (first entry)
 XX Cyclin-dependent kinase modulation biomarker SEQ ID NO 542.
 DE cyclotatic; cyclin-dependent kinase; cdk; biomarker.
 KW Homo sapiens.
 OS W02005012875-A2.
 PN 10-FEB-2005.
 PD 29-JUL-2004; 2004WO-US024424.
 PF 29-JUL-2003; 2003US-0490890P.
 PR (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 DR WPI; 2005-163068/17.
 DR N-PSDB; ADX05976.

XX Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.
 XX Claim 5; SEQ ID NO 542; 141pp; English.

XX This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2174 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[15-(1,1-Dimethylethyl)-2-
 CC oxazolyl]methylthiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct sequences. This
 CC sequence represents a biomarker used in the method of the invention.
 XX
 SQ Sequence 542 AA;
 Query Match 99.8%; Score 2873; DB 9; Length 542;
 Best Local Similarity 99.8%; Pred. No. 1e-264; Mismatches 1; Indels 0; Gaps 0;
 Matches 541; Conservative 0;
 QY 1 MBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLOISNGTSSVIVS 60
 DB 1 MBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLOISNGTSSVIVS 60
 QY 61 RRPSEGNVQKEDKICIKYFDQWSSDQVEFVEHLISRMCHYOHGHINLYLKPMLORDFI 120
 DB 61 RRPSEGNVQKEDKICIKYFDQWSSDQVEFVEHLISRMCHYOHGHINLYLKPMLORDFI 120
 QY 121 TALPEOGLDHI AENILSYLDARS LCAAE LVCKEWQ RVI SEGM LKKLI ERMV RTDPLWK G 180
 DB 121 TALPEOGLDHI AENILSYLDARS LCAAE LVCKEWQ RVI SEGM LKKLI ERMV RTDPLWK G 180
 QY 181 LSERRGWDQYLFKNRPTDGP PNFYSRSLYPKIIQDIETIESNWRGCRHNLQRIQCRSENS 240
 DB 181 LSERRGWDQYLFKNRPTDGP PNFYSRSLYPKIIQDIETIESNWRGCRHNLQRIQCRSENS 240
 QY 241 KGVYCLQYDDEKII SGLRDN SIKINDKTSLECLKVL TGTG SVLCLOYDERVIVTGS S DS 300
 DB 241 KGVYCLQYDDEKII SGLRDN SIKINDKTSLECLKVL TGTG SVLCLOYDERVIVTGS S DS 300
 QY 301 TVRVWDVNTGEVLNTLIHNEAVLHFRFNSGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
 DB 301 TVRVWDVNTGEVLNTLIHNEAVLHFRFNSGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
 QY 361 GHRAAVNVVDFDDKYIVSASGDRRTIKVWSTSTCEVFTLNGHKGRIACIQYRDLRVVSGS 420
 DB 361 GHRAAVNVVDFDDKYIVSASGDRRTIKVWSTSTCEVFTLNGHKGRIACIQYRDLRVVSGS 420
 QY 421 SDNTIRLWDIECGACLRVLEGGHEELVRCIRFNDKRIVSGAYDGKIIVWDLQAALDPRAPA 480
 DB 421 SDNTIRLWDIECGACLRVLEGGHEELVRCIRFNDKRIVSGAYDGKIIVWDLQAALDPRAPA 480
 QY 481 STLCRLTLVEHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSRPTTYI 540
 DB 481 STLCRLTLVEHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSRPTTYI 540
 QY 541 SR 542
 DB 541 SR 542

RESULT 8
 ADX88282
 ID ADX88282 standard; protein; 563 AA.
 XX ADX88282;
 AC ADX88282;
 DT 18-NOV-2004 (first entry)
 DE Human protein of a TNF-alpha signalling pathway protein complex Seq 137.
 XX
 KW protein complex; tumour necrosis factor-alpha signalling pathway;
 KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
 KW inflammatory bowel disease; infectious disease; septic shock;
 KW bacterial infection; neurological disease; stroke-induced inflammation;
 KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
 KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
 XX Homo sapiens.
 OS W02004035783-A2.
 PN 29-APR-2004.
 PD 29-APR-2004.
 XX

PF 24-SEP-2003; 2003WO-EP050655.
 XX
 PR 26-SEP-2002; 2002EP-00021809.
 PR 10-FEB-2003; 2003EP-00100274.
 XX
 PA (CELL-) CELLZOME AG.
 XX
 XX Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
 PI Superti-Furga G, Kruse U;
 PI WPI; 2004-348460/32.
 XX
 XX New protein complex comprising at least one first and second protein of
 PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
 PT diagnosing or treating inflammation, neurological diseases, infectious
 PT diseases or cancer.
 XX
 XX Example; SEQ ID NO 137; 1980pp; English.
 XX
 XX This invention relates to novel protein complexes of the tumour necrosis
 CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
 CC methods for preparing these complexes comprising at least two component
 CC proteins, as well as screening methods to identify modulators of the
 CC pathway, which include antibodies, agonists and antagonists thereof. The
 CC present invention describes a protein complex and kit that are useful for
 CC diagnosing, prognosing or treating chronic inflammatory diseases such as
 CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
 CC such as septic shock and bacterial infections; neurological diseases such
 CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
 CC cancer. Accordingly, these complexes can be used for the development of
 CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
 CC antirheumatic, cytostatic and antibacterial activities and can be used
 CC for gene therapy purposes. In particular, the invention further provides
 CC siRNA-oligonucleotides useful for inhibiting protein expression for in
 CC vitro or cell culture assays. This polypeptide is a human protein that
 CC can be used in combination with other proteins provided in the
 CC specification to form novel complexes of the TNF-alpha signalling pathway
 CC of the invention.
 XX
 XX Sequence 563 AA;
 SQ
 Query Match 95.7%; Score 2755.5; DB 8; Length 563;
 Best Local Similarity 93.3%; Pred. No. 1.8e-253;
 Matches 525; Conservative 2; Mismatches 15; Indels 21; Gaps 1;
 QY 1 MEPSDVIEDKTIELMCSVPRSLMIGCANLVESMCALSCLOSMPSVRCL----- 48
 DB 1 MEPSDVIEDKTIELMCSVPRSLMIGCANLVESMCALSCLOSMPSVRCLQNTSVMEDQNE 60
 QY 49 -----QISNCTSSVIVSRKPSGNYQKEKDLCKYFDOWSESDQVEFVEHLISRM 99
 DB 61 ESPKKSALWQISNGTSSVIVSRKRPSEGNQYQKEKDLCKYFDOWSESDQVEFVEHLISRM 120
 QY 100 CHVOGHINSYLPKMLQDRTITALPEOGLDHIAENILSYLDARSLCAELVCKEWRQVIS 159
 DB 121 CHVOGHINSYLPKMLQDRTITALPEOGLDHIAENILSYLDARSLCAELVCKEWRQVIS 180
 QY 160 EGMWLKLLIERWVRTDPLWGLSERRGWDQYLFKNRPTDGPNSFYRSLPKIIDIETI 219
 DB 181 EGMWLKLLIERWVRTDPLWGLSERRGWDQYLFKNRPTDGPNSFYRSLPKIIDIETI 240
 QY 220 ESNWRCGRHNLQRIQCSSENSKVYCYLOYDDEKILSGLRDINSIKWPKLSLECLKVLGTG 279
 DB 241 ESNWRCGRHNLQRIQCSSENSKVYCYLOYDDEKILSGLRDINSIKWPKLSLECLKVLGTG 300
 QY 280 TGSVLCLQYDERVIVTGSSTVRVMDVNTGEVLTILHNEAVLHLRFNGLMVTCSKD 339
 DB 301 TGSVLCLQYDERVIVTGSSTVRVMDVNTGEVLTILHNEAVLHLRFNGLMVTCSKD 360
 QY 340 RSIADVMDASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWSTSTCEFVRTL 399
 DB 361 RSIADVMDAFCHRVHFFPCGWPRAAVNVVDFDDKYIVSASGDRITIKWSTSTCEFVRTL 420

400 NGHKRGIAQLQYRDRLVWVGSSDNTIRLWDIEGACALRVLEGHHEELVRCIRFNDKRIVSG 459
 DB 421 NGHKRGIAQLQYRDRLVWVGSSDNTIRLWDIEGACALRVLEGHHEELVRCIRFNDKRIVSG 480
 QY 460 AYDGKIKVWDLOAALDPRAPASTLCRLTVEHSGRVFRLQFDFQIISSSHDDTILWDF 519
 DB 481 AYDGKIKVWDLOAALDPRAPASTLCRLTVEHSGRVFRLQFDFQIISSSHDDTILWDF 540
 QY 520 LNVPPSAQNETRSPSRITYTYISR 542
 DB 541 LNVPPSAQNETRSPFRITYTYISR 563

RESULT 9
 ADX05979
 ID ADX05979 standard; protein; 529 AA.
 XX
 AC ADX05979;
 XX
 XX 21-APR-2005 (first entry)
 DT
 DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 544.
 DE
 XX cytostatic; cyclin-dependent kinase; cdk; biomarker.
 KW
 XX Homo sapiens.
 OS
 XX W02005012875-A2.
 PN
 XX 10-FEB-2005.
 PD
 XX 29-JUL-2004; 2004WO-US024424.
 PF
 XX 29-JUL-2003; 2003US-0490990P.
 PR
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 PI WPI; 2005-163068/17.
 DR N-PSDB; ADX05978.
 XX
 XX Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.
 PT
 PS Claim 5; SEQ ID NO 544; 141pp; English.
 XX
 XX This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-oxazolylmethyl)thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This sequence represents a biomarker used in the method of the invention.
 XX
 XX Sequence 529 AA;
 SQ
 Query Match 92.6%; Score 2666.5; DB 9; Length 529;
 Best Local Similarity 92.4%; Pred. No. 5.2e-245;
 Matches 512; Conservative 1; Mismatches 4; Indels 37; Gaps 3;

QY	1	MEPDSVIEDKTIELM-CSV-----PRSLWLGCANLVESMCALSCLOSMPSVRCL	48
Db	1	MEPDSVIEDKTIELMTSVMEQNEDESFKNTLM-----	35
QY	49	QISNGTSSVIVSRKRPSEGNQYKEDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHIN	108
Db	36	QISNGTSSVIVSRKRPSEGNQYKEDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHIN	95
QY	109	SYLKPMQLQDFITALPEQGLDHTAENILSYLDARSLCAAELVCKEWRVISEGMLWKLI	168
Db	96	SYLKPMQLQDFITALPEQGLDHTAENILSYLDARSLCAAELVCKEWRVISEGMLWKLI	155
QY	169	ERMVRTDPLWKLSESRGWDOYLFKNRPTDGPNSFYRSLPKIIODIETISNWRRCGRH	228
Db	156	ERMVRTDPLWKLSESRGWDOYLFKNRPTDGPNSFYRSLPKIIODIETISNWRRCGRH	215
QY	229	NLQRIQCRSENSGVVYCLOYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLCLO	288
Db	216	NLQRIQCRSENSGVVYCLOYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLCLO	275
QY	289	DERVIVITGSSDSVTRVMDVNTGEVLNTLIHNEAVLHFRFNSGLMVTCSKDRSIAVWMA	348
Db	276	DERVIVITGSSDSVTRVMDVNTGEVLNTLIHNEAVLHFRFNSGLMVTCSKDRSIAVWMA	335
QY	349	SATDITLRLVVGHRAAVNVDPDDKYIVSASGDRTIKVMSTSTCFVRTLNGHKGRIAC	408
Db	336	SATDITLRLVVGHRAAVNVDPDDKYIVSASGDRTIKVMSTSTCFVRTLNGHKGRIAC	395
QY	409	LQYRDLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKW	468
Db	396	LQYRDLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKW	455
QY	469	DLQAALDPRAPASTLCLRTLVEHSGRVFRLOFDEFQIISSSHDDTILIWDFLNVPPSAQN	528
Db	456	DLQAALDPRAPASTLCLRTLVEHSGRVFRLOFDEFQIISSSHDDTILIWDFLNVPPSAQN	515
QY	529	ETRSRPTTYIYSR 542	
Db	516	ETRSRPTTYIYSR 529	
RESULT 10			
ID	ADX05981	standard; protein; 508 AA.	
XX	AC	ADX05981;	
XX	AC	ADX05981;	
DT	21-APR-2005	(first entry)	
XX	DE	Cyclin-dependent kinase modulation biomarker SEQ ID NO 546.	
XX	DE	cytostatic; cyclin-dependent kinase; cdk; biomarker.	
XX	KW	Homo sapiens.	
OS	XX		
PN	XX	WO2005012875-A2.	
XX	XX	10-FEB-2005.	
PF	XX	29-JUL-2004; 2004WO-US024424.	
XX	XX	29-JUL-2003; 2003US-0490890P.	
PR	XX	(BRIM) BRISTOL-MYERS SQUIBB CO.	
PA	XX		
PI	XX	Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;	
XX	XX	WPI; 2005-163068/17.	
DR	XX	N-PSDB; ADX05980.	
XX	XX	Biomarkers useful for predicting or determining the response of a mammal	
PT	XX	to a cancer treatment comprising administration of a modulator of cyclin-	

PT	XX	dependent kinase activity.	
PS	XX	Claim 5; SEQ ID NO 546; 141pp; English.	
XX	XX	This invention describes a novel method of predicting or determining	
CC	CC	whether a mammal will respond or is responding to an anti-cancer agent	
CC	CC	that modulates cyclin-dependent kinase (cdk) activity. The method	
CC	CC	comprises measuring the level of one or more biomarkers selected from	
CC	CC	2774 biomarkers given in the specification (nucleotide sequence SEQ ID	
CC	CC	NO:1246 (Genbank EST W28729) is especially preferred). The method of the	
CC	CC	invention is utilized in a kit for determining or predicting whether	
CC	CC	patient would be susceptible or resistant to treatment by an agent	
CC	CC	modulating cdk activity. The invention also describes a method for	
CC	CC	utilizing individualized genetic profiles for treating diseases and	
CC	CC	disorders based on patient's response and molecular level, specialized	
CC	CC	microarrays comprising the biomarkers described, antibodies directed	
CC	CC	against the biomarkers and a cell culture model to identify biomarkers.	
CC	CC	The cdk modulator is preferably N-5-([5-(1,1-Dimethylethyl)-2-	
CC	CC	oxazolyl]methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-	
CC	CC	tartaric acid salt. Note: The sequence data for this patent did not form	
CC	CC	part of the printed specification, but was obtained in electronic format	
CC	CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This	
CC	CC	sequence represents a biomarker used in the method of the invention.	
XX	XX	Sequence 508 AA;	
SQ	SQ		
Query Match 92.4%; Score 2661; DB 9; Length 508;			
Best Local Similarity 93.5%; Pred. No. 1.6e-244;			
Matches 507; Conservative 0; Mismatches 1; Indels 34; Gaps 1;			
QY	1	MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLQISNGTSSVIVS	60
Db	1	MEPDSVIEDKTIELM-----ISNGTSSVIVS 26	
QY	61	RRRPSEGNQYKEDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINLYKPMQLQDFI	120
Db	27	RRRPSEGNQYKEDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINLYKPMQLQDFI	86
QY	121	TALPEQGLDHTAENILSYLDARSLCAAELVCKEWRVISEGMLWKLIERMVRTDPLWKG	180
Db	87	TALPEQGLDHTAENILSYLDARSLCAAELVCKEWRVISEGMLWKLIERMVRTDPLWKG	146
QY	181	LSERRGMDOYLFKNRPTDGPNSFYRSLPKIIQDIETIESNWRRCGRHNLQRIQCRSENS	240
Db	147	LSERRGMDOYLFKNRPTDGPNSFYRSLPKIIQDIETIESNWRRCGRHNLQRIQCRSENS	206
QY	241	KGVCICLYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLCLOYDERVIVTSSDS	300
Db	207	KGVCICLYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLCLOYDERVIVTSSDS	266
QY	301	TVRVMDVNTGEVLNTLIHNEAVLHFRFNSGLMVTCSKDRSIAVWDMASATDITLRLVLV	360
Db	267	TVRVMDVNTGEVLNTLIHNEAVLHFRFNSGLMVTCSKDRSIAVWDMASATDITLRLVLV	326
QY	361	GHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCFVRTLNGHKGRIACLOYRDLRVVSGS	420
Db	327	GHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCFVRTLNGHKGRIACLOYRDLRVVSGS	386
QY	421	SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVMDLQAALDPAPA	480
Db	387	SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVMDLQAALDPAPA	446
QY	481	STLCLRTLVEHSGRVFRLOFDEFQIISSSHDDTILIWDFLNVPPSAQNTRSPRTTYI	540
Db	447	STLCLRTLVEHSGRVFRLOFDEFQIISSSHDDTILIWDFLNVPPSAQNTRSPRTTYI	506
QY	541	SR 542	
Db	507	SR 508	
RESULT 11			
AAW78583			

DB	AAAM78583	standard; protein; 579 AA.
DB	AAAM78583	
DB	06-NOV-2001	(first entry)
DB	Human protein	SEQ ID NO 1245.
DB	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.	
DB	Homo sapiens.	
DB	WO200157190-A2.	
DB	09-AUG-2001.	
DB	05-FEB-2001;	2001WO-US004098.
DB	03-FEB-2000;	2000US-00496914.
DB	27-APR-2000;	2000US-00560875.
DB	20-JUN-2000;	2000US-00598075.
DB	19-JUL-2000;	2000US-00620325.
DB	01-SEP-2000;	2000US-00654936.
DB	15-SEP-2000;	2000US-00663561.
DB	20-OCT-2000;	2000US-00693325.
DB	30-NOV-2000;	2000US-00728422.
DB	(HYSE-) HYSEQ INC.	
DB	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;	
DB	Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;	
DB	Xue AJ, Yang Y, Wejhrman T, Goodrich R;	
DB	WPI; 2001-476283/51.	
DB	N-PSDB; AAK51716.	
DB	Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.	
DB	Claim 20; Page 3504-3505; 6221pp; English.	
DB	The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAAM78323-AAAM80302) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Notes: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication	
DB	Sequence 579 AA;	
DB	Query Match	85.4%; Score 2458.5; DB 4; Length 579;
DB	Best Local Similarity	79.1%; Pred. No. 4.3e-225;
DB	Matches 458; Conservative	49; Mismatches 35; Indels 37; Gaps 4;
DB	1 MEP-DSVIEDKTIELMCSVPRLMGLCANLVESMCALSCL	----- 39
DB	1 MDPAEVLQERALKFMCMPRLMGLCSSLADSPSLRCLNPGTALTAFTQYNSCARL	60
DB	40 -----QSMPSVRLCL---QISNGTSSVIVSRKRPSEGNQKEKDLCKYFDQWSE	85
DB	61 CLNQETVCLASTAMKTCNVAKTKLANGTSSMIVPKQKLSAYEKEKELCVKTFEQWSE	120
DB	86 SDQVEFVEHLISRMCHYQHGHINSYLPKMLQDFITALPEQGLDHAENILSYLDAKSLC	145
DB	121 SDQVEFVEHLISQCHYQHGHINSYLPKMLQDFITALPEQGLDHAENILSYLDAKSLC	180
DB	146 AAEVCKEWRVISEGMLWKKLIERMYRTDPLWKLSEKRGWQYLFKNRPTDG--PPNS	203
DB	181 AAEVCKEWRVITSDGMLWKKLIERMYRTDPLWKLSEKRGWQYLFKNRPTDG--PPNS	240
DB	204 FYRSLYPKIIQDIETIESNWRGRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRDSIK	263
DB	241 FYRALYPKIIQDIETIESNWRGRHSLQRIHCRSETSGVYCLQYDQKIVSGLRDNTIK	300
DB	264 IWKTSLECKLVLTGHTGSLVCLQYDERVITGSSDSTVRVWVNTGEVLTNLHNEAV	323
DB	301 IWKNLTLECKRIILTGTGSLVCLQYDERVITGSSDSTVRVWVNTGEVLTNLHNEAV	360
DB	324 LHLRFSNGLMVTCKDERSIAVWDMASATDITLRLVVGHRAAVNVVDFDDKIVIVSASGDR	383
DB	361 LHLRFNNGMMVTCKDERSIAVWDMASPTDITLRLVVGHRAAVNVVDFDDKIVIVSASGDR	420
DB	384 TIKWSTSTCEVFRTLNHKGRIACQYRDLRVVVGSSDNTIRLWDIECGACLRVLEGHE	443
DB	421 TIKWNTSTCEVFRTLNHKGRIACQYRDLRVVVGSSDNTIRLWDIECGACLRVLEGHE	480
DB	444 ELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCRLTVLHSGRVFRLQDFEF	503
DB	481 ELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCRLTVLHSGRVFRLQDFEF	540
DB	504 QIITSSSHDDTILWDLFNLVPPSAQNETRSPSRVITYISR	542
DB	541 QIVSSSHDDTILWDLFNLVPPSAQNETRSPSRVITYISR	579
DB	RESULT 12	
DB	AAAM78582	
DB	ID	AAAM78582 standard; protein; 605 AA.
DB	AC	AAAM78582;
DB	AC	AAAM78582;
DB	06-NOV-2001	(first entry)
DB	Human protein	SEQ ID NO 1244.
DB	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.	
DB	Homo sapiens.	
DB	WO200157190-A2.	
DB	09-AUG-2001.	
DB	05-FEB-2001;	2001WO-US004098.
DB	03-FEB-2000;	2000US-00496914.
DB	27-APR-2000;	2000US-00560875.
DB	20-JUN-2000;	2000US-00598075.
DB	19-JUL-2000;	2000US-00620325.
DB	01-SEP-2000;	2000US-00654936.
DB	15-SEP-2000;	2000US-00663561.
DB	20-OCT-2000;	2000US-00693325.
DB	30-NOV-2000;	2000US-00728422.
DB	(HYSE-) HYSEQ INC.	
DB	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;	
DB	Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;	
DB	Xue AJ, Yang Y, Wejhrman T, Goodrich R;	
DB	WPI; 2001-476283/51.	
DB	N-PSDB; AAK51715.	

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 XX
 PS Claim 20; Page 3503-3504; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 605 AA;

Query Match 84.9%; Score 2445.5; DB 4; Length 605;
 Best Local Similarity 75.7%; Pred. No. 8e-224;
 Matches 458; Conservative 49; Mismatches 35; Indels 63; Gaps 4;
 QY 1 MEP-DSVIEDKTIELMCSVPRSLWLGCAINLVESMCALSCL----- 39
 Db 1 MDPAEAVLQEKALKFMCSPRSLWLGCSLADSMPSRLCLYNPGTGALTAFMNSSREDC 60
 QY 40 -----QSMPSVRCL---QISNGTSSVIV 59
 Db 61 NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTCNCVAKTKLANGTSSMIV 120
 QY 60 SRKRPSCGYKEDKLCIKFYDOWSESDQVEFVHILISRMCHYQHGHINSYLPKMLQORDF 119
 Db 121 PKQKLSASVEKEKELCVKFEQWSESDQVEFVHILISQCHYQHGHINSYLPKMLQORDF 180
 QY 120 ITALPEOGLDHIAENILSYLDARSLCAAEVLCKEWMORVISEGMLWKKLIERMVTRDPLWK 179
 Db 181 ITALPARGLDHIAENILSYLDARSLCAAEVLCKEWMORVISEGMLWKKLIERMVTRDPLWK 240
 QY 180 GLSERGWDYLFKNRPTDG--PNSFYRSLYPKIIDIETIESNRCGRHNLQRCRS 237
 Db 241 GLAERRGWGYLFPKNKPPDGNAPNSFYRALYPKIIDIETIESNRCGRHNLQRCRS 300
 QY 238 ENSKGVVCLQYDDQKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVCLQYDERVITGS 297
 Db 301 ETSKGVVCLQYDDQKIVSGLRDNITIKIWDKNTLECKRILGTGHTGSLVCLQYDERVITGS 360
 QY 298 SDSTVRVMDVNTGEVMTLIIHNEAVLHFRSNGLMVTCSDRSIAVWDMASATDITLRR 357
 Db 361 SDSTVRVMDVNTGEVMTLIIHNEAVLHFRSNGLMVTCSDRSIAVWDMASATDITLRR 420
 QY 358 VLVGHRAAVNVDPDDKIVYASGDRTIKWMTSTCFEFTLVNKGKGIACLOYRDLVV 417
 Db 421 VLVGHRAAVNVDPDDKIVYASGDRTIKWMTSTCFEFTLVNKGKGIACLOYRDLVV 480
 QY 418 SGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGIKIVWDIQAALDPR 477
 Db 481 SGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGIKIVWDIQAALDPR 540
 QY 478 APASTLCRLTVEHSGRVFRQLQDFEQIISSHDDTILIWDFLNVPPSAQNETRSPRTY 537
 Db 541 APAGTLCRLTVEHSGRVFRQLQDFEQIISVSSSHDDTILIWDFLNDPAQAAPRSPRTY 600
 QY 538 TYISR 542
 Db 601 TYISR 605

RESULT 13
 ADS88274
 ID ADS88274 standard; protein; 605 AA.

XX ADS88274;
 AC
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human protein of a TNF-alpha signalling pathway protein complex Seq 129.
 XX
 KW protein complex; tumour necrosis factor-alpha signalling pathway;
 KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
 KW inflammatory bowel disease; infectious disease; septic shock;
 KW bacterial infection; neurological disease; stroke-induced inflammation;
 KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
 KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035783-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 24-SEP-2003; 2003WO-EP050655.
 PR 26-SEP-2002; 2002EP-00021809.
 PR 10-FEB-2003; 2003EP-00100274.
 XX
 PA (CELL-) CELLZONE AG.
 XX
 PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
 PI Superti-Furga G, Kruse U;
 XX
 DR WPI; 2004-348460/32.
 XX
 PT New protein complex comprising at least one first and second protein of
 PT the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for
 PT diagnosing or treating inflammation, neurological diseases, infectious
 PT diseases or cancer.
 XX
 PS Example; SEQ ID NO 129; 1980pp; English.
 XX
 CC This invention relates to novel protein complexes of the tumour necrosis
 CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
 CC methods for preparing these complexes comprising at least two component
 CC proteins, as well as screening methods to identify modulators of the
 CC pathway, which include antibodies, agonists and antagonists thereof. The
 CC present invention describes a protein complex and kit that are useful for
 CC diagnosing, prognosing or treating chronic inflammatory diseases such as
 CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
 CC such as septic shock and bacterial infections; neurological diseases such
 CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
 CC cancer. Accordingly, these complexes can be used for the development of
 CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
 CC antirheumatic, cytostatic and antibacterial activities and can be used
 CC for gene therapy purposes. In particular, the invention further provides
 CC siRNA-oligonucleotides useful for inhibiting protein expression for in
 CC vitro or cell culture assays. This polypeptide is a human protein that
 CC can be used in combination with other proteins provided in the
 CC specification to form novel complexes of the TNF-alpha signalling pathway
 CC of the invention.
 XX
 SQ Sequence 605 AA;

Query Match 84.9%; Score 2445.5; DB 8; Length 605;
 Best Local Similarity 75.7%; Pred. No. 8e-224;
 Matches 458; Conservative 49; Mismatches 35; Indels 63; Gaps 4;
 QY 1 MEP-DSVIEDKTIELMCSVPRSLWLGCAINLVESMCALSCL----- 39
 Db 1 MDPAEAVLQEKALKFMCSPRSLWLGCSLADSMPSRLCLYNPGTGALTAFQNSSREDC 60
 QY 40 -----QSMPSVRCL---QISNGTSSVIV 59
 Db 61 NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTCNCVAKTKLANGTSSMIV 120

Query Match	84.2%	Score 2423	DB 4	Length 654
Best Local Similarity	72.5%	Fred. No. 1.3e-221		
Matches 458	Conservative 49	Mismatches 35	Indels 90	Gaps 5
QY	1	MEP-DSVIEDKTIELM	-----CSVPSRLMLGCANLVES	32
		: : : : :	: : : : : :	
DB	23	MDPAEAVLQEKALFKMF	TSRVQCSMPRSLMLGCSSLADS	82
		-----	-----	
QY	33	MCALSSCL	-----	39

PI¹ Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

RESULT 15
AAM79567

ID AAM79567 standard; protein; 654 AA.

XX AC AAM79567;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 3213.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US004098.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PR 20-JUN-2000; 2000US-00598075.

XX PR 19-JUL-2000; 2000US-00620325.

XX PR 01-SEP-2000; 2000US-00654936.

XX PR 15-SEP-2000; 2000US-00663561.

XX PR 20-OCT-2000; 2000US-00693325.

XX PR 30-NOV-2000; 2000US-00728422.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX WPI: 2001-476283/51.

XX N-PSDB: AAK52700.

XX PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.

XX PS Claim 20; Page 286; 6221pp; English.

XX CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication

XX SQ Sequence 654 AA;

Query Match 84.2%; Score 2423; DB 4; Length 654;
Best Local Similarity 72.5%; Pred. No. 1.3e-21;
Matches 458; Conservative 49; Mismatches 35; Indels 90; Gaps 5;

Qy 1 MEP-DSVIEDKTIELM-----CSVPRSLWLGCANLIVES 32

Db 23 MDPAAVLQEKALFMFRSWCPGWNMTMARSRLTATSTRVQCSPRSLWLGCSLADS 82

Qy 33 MCALSCL----- 39

Db	83	MESLRCLYNPGTGALTAFQNSSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNQETV	142
Qy	40	-----QSMPSVRCL-----QISNGTSSVIVSRKRPSSENGYKEKDLCKIKYFDQWSESQVFEV	92
Db	143	CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKELCVKYPEQWSESQVFEV	202
Qy	93	EHLISRMCHYQHGHINSYLPKMLQRFITALPEQGLDHTAENILSYLDARSICAAELVCK	152
Db	203	EHLISQMHYQHGHINSYLPKMLQRFITALPARGLDHTAENILSYLDARSICAAELVCK	262
Qy	153	EWQRVISEGLMKWKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYP	210
Db	263	EWYRTSDGMLWKLIERMVRTDSLWRGLAERRGWQYLFKNKPPDGNAPPNSFYREALYP	322
Qy	211	KIIQDIETIESNWRGCRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRNSIKIWDKTSL	270
Db	323	KIIQDIETIESNWRGCRHSLQRIHCRSETSGVYCLQYDDQKIVSGLRNTTIKWDKNTL	382
Qy	271	ECLKVLTGHTGSVLCLOYDERVIVTGSSDSTVRVMDVNTGEVNTLIHHEAVLHURFEN	330
Db	383	ECKRILTGHTGSVLCLOYDERVIVITGSSDSTVRVMDVNTGEMNTLIHHEAVLHURFNN	442
Qy	331	GLMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWST	390
Db	443	GMVVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWNT	502
Qy	391	STCEFVRTLNHGKRGIAQLQYDRDLVWVGSSDNTIRLWDIECGACLRVLEGHEELVRCIR	450
Db	503	STCEFVRTLNHGKRGIAQLQYDRDLVWVGSSDNTIRLWDIECGACLRVLEGHEELVRCIR	562
Qy	451	FDNKRIVSGAYDGKIKVWDLQALDPAPASTLCRLTLVEHSGRVFRLQDFDEFOIIVSSH	510
Db	563	FDNKRIVSGAYDGKIKVWDLVAALDPAPAGTLCRLTLVEHSGRVFRLQDFDEFOIIVSSH	622
Qy	511	DTILIWDFLNVPPSAQNETRSPSRITYYISR	542
Db	623	DTILIWDFLNDPAAQSEPPRSPRITYYISR	654

Search completed: August 25, 2006, 07:17:19

Job time : 198 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:17:37 ; Search time 41 Seconds
(without alignments)
1271.939 Million cell updates/sec

Title: US-10-665-715-16
Perfect score: 2879
Sequence: 1 MEPDSVIEDKTIELMCSVPR.....PPSAQNTRSPSRTYIISR 542

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2301	79.9	518	B48088	beta-transducin re
2	1638.5	56.9	701	T18607	hypothetical prote
3	683.5	23.7	506	T50211	WD-repeat protei
4	584	20.3	605	T38932	probable sulfur me
5	538	18.7	640	S49932	MET30 protein - ye
6	525	18.2	650	T46660	sulfur controller-
7	516.5	17.9	267	S62507	hypothetical trp-a
8	512	17.8	579	T22703	hypothetical prote
9	468.5	16.3	1356	T18521	beta transducin-l1
10	453	15.7	775	T45136	WD repeat protei
11	425	14.8	1227	AE1810	WD-40 repeat prote
12	418	14.5	779	S56245	cell division cont
13	389.5	13.5	703	T43557	F-box/WD-repeat pr
14	387.5	13.5	1189	A12493	WD-repeat protei
15	383.5	13.3	1747	AC1842	WD-40 repeat prote
16	378.5	13.1	1258	AC12155	WD-repeat protei
17	377.5	13.1	1526	A12239	WD-40 repeat prote
18	374	13.0	1683	AF7071	WD-40 repeat prote
19	360.5	12.5	677	AE1861	serine/threonine k
20	359.5	12.5	559	AB2202	hypothetical prote
21	347	12.1	1711	AD1842	WD-40 repeat prote
22	343	11.9	409	S36113	Lis-1 protein - hu
23	343	11.9	410	S48052	platelet-activatin
24	343	11.9	1146	A55532	myosin-heavy-chain
25	340.5	11.8	777	T41075	hypothetical WD-re
26	340	11.8	515	S19487	hypothetical prote
27	339	11.8	676	AH2195	hypothetical prote
28	329.5	11.4	317	T46032	WD-40 repeat regul
29	323	11.2	333	G85034	probable WD-repeat

ALIGNMENTS

RESULT 1

B48088

beta-transducin repeat-containing protein - African clawed frog

N:Alternate names: beta-Trcp

C:Species: Xenopus laevis (African clawed frog)

C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: B48088

R:Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.

Mol. Cell. Biol. 13, 4953-4966, 1993

A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase arr

A:Reference number: A48088; MUID:93330289; PMID:8393141

A:Accession: B48088

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-518 <SP>

A:Cross-references: UNIPROT:Q91854; UNIPARC:UPI0000137338; GB:M98268; NID:G295542; PIDN

C:Keywords: duplication

F:431-462/Domain: WD repeat homology <WD1>

Query Match	79.9%	Score	2301;	DB	2;	Length	518;
Best Local Similarity	88.0%;	Pred. No.	1.9e-166;				
Matches	424;	Conservative	33;	Mismatches	23;	Indels	2;
Gaps	1;						
QY	44	SVRCIQISNGTSSVTVSRKRPSEGNVQKEKDLCKYFDQWSSDOVEFVHEHLISRMCHYQ	103				
Db	34	TLRQTKLANGSSMIVPKQKLSANYEKEKELCVKIFQWSECDQVFEVHEHLISRMCHYQ	93				
QY	104	HGHINSYLPKMLQRFITALPEQGLDHAENILSYLDARSLCAELVCKEWRVISEGML	163				
Db	94	HGHINTYLPKMLQRFITALPARGLDHAENILSYLDARSLCAELVCKEWRVISEGML	153				
QY	164	WKKLIERMVRTDPLWKGLSERGWQYLFQKRPDGTG--PPNSFYRSLVPKIIQDIETIES	221				
Db	154	WKKLIERMVRTDPLWKGLSERGWQYLFQKRPDGTG--PPNSFYRSLVPKIIQDIETIES	213				
QY	222	NWRCGRHNLRIQCHSENSKGVYCLQYDDEKTIISGLRNSIKWDKTSLECLKVLGTHTG	281				
Db	214	NWRCGRHNLRIQCHSENSKGVYCLQYDDEKTIISGLRNSIKWDKTSLECLKVLGTHTG	273				
QY	282	SVLCIQYDERVITVTSSDSTVRVMDVNTGEVLNTLIHNEAVLHLRFNSGLMVTCKDORS	341				
Db	274	SVLCIQYDERVITVTSSDSTVRVMDVNTGEVLNTLIHNEAVLHLRFNSGLMVTCKDORS	333				
QY	342	IAVMDASATITLRLRVLVGHRAAANNVVDFFDKYIVSASGDRFTIKVNSTSTCEPVRTLLG	401				
Db	334	IAVMDASATITLRLRVLVGHRAAANNVVDFFDKYIVSASGDRFTIKVNSTSTCEPVRTLLG	393				
QY	402	HKRGACIQYDRDLVVGSSDNTIRLWDIECGACLRVLEGGHEELVRCIRFDNKNRIVSGAY	461				
Db	394	HKRGACIQYDRDLVVGSSDNTIRLWDIECGACLRVLEGGHEELVRCIRFDNKNRIVSGAY	453				
QY	462	DGKIKVWDLQAALDPRAPASTLCRLTVLVEHSGRVPRLOFDFEQIISSSHDDTLILWDFLN	521				

Best Local Similarity 30.6%; Pred. No. 2.7e-36;
Matches 147; Conservative 85; Mismatches 167; Indels 82; Gaps 11;

Qy 108 NSYLKPMQLRDFITALPEQGLDHAENILSYLDARSICAAELCKEQRVISEGMLWKKL 167
:
Db 98 SSTLDSLVRDLFLSLPVE---ISPRLSFLDSLRSCQAQQSVKHWEKADDDVIWHRM 153

Qy 168 IER-----MVTDPFLWKCLSE-----RRGWDOY-----LPFNPTDG 199
:
Db 154 CEQHINRKCEKGWGLPLLERNTLYAKASIQRYERLTGRGVDOAHESSPVKAKLDDY 213

Qy 200 P-----PNSFVSRLYP-----KIIDIETIESNWRRCGRHNLRIQCR- 236
:
Db 214 PTGSNEETISSVPPSPNSOSKFPLPKTPRWKEVAERCRCVENRHGR-----CRQ 266

Qy 237 ---SENSKGYVCLOYYDDDEKIIISGLRDNSIKIMDKTSLECIKVLGTGSGVLCQYDERVI 293
:
Db 267 VVLSGHSDGVMCQLVNRNILASGYDATIRLNWLATFOQVALLEGHSSGVTCLQFDQCKL 326

Qy 294 VTGSSGSTVRVDNVNTGEVNTLIHHNEAVLHLRFPSNGLMTVCSKDRSIAVDMASATDI 353
:
Db 327 ISGSMDKTIRIWNRTSETCISIILHGHTDTSVLCITFTDTLLVSGSADCTVXLMHFSGSKRI 386

Qy 354 TLARLVGHRAAANNVDF--DDKYIVVASGDRTIKWSTSTCFVRTLNGHKRGIAQLQY 411
:
Db 387 TLR----GHTGPVNSVRIRIDRGLVLSGSDSTIKIWSLETNCLHTFSAHIGPVQSAL 442

Qy 412 RDLRLWVGSSDNTIRLWDIECGACLRVLEGGHEELVRCIRFPDNKRIVSGAYDGIKWIDLQ 471
:
Db 443 ADRLPFCSDLGTIKQWDIEKKCVHTLFHIGEWELIADHLRLISGAHDGVVQWVE-- 500

Qy 472 AALDPRAPASTCLRILTIVEHSRVRFRLOQDFEQIISSSHDDTLIWDFLNPVPSAQNETR 531
:
Db 501 -----ACECVHTLKNSHPVTSVALGDCVWVGSEDGKIYLMFNAPNESPVSTQ 551

Qy 532 S 532
|
Db 552 S 552

RESULT 5
S49932
METJ30 protein - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein Y1905.02; protein YIL046w
C;Species: *Saccharomyces cerevisiae*
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 05-Oct-2004
C;Accession: S49932; S43750
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, December 1994
A;Reference number: S49931
A;Accession: S49932
A:Molecule type: DNA
A;Residues: 1-640 <ODE>
A;Cross-references: UNIPROT:P39014; UNIPARC:UPI0000012F726; GB:Z47047; EMBL:Z46861; NID:S49932
R;Thomas, D.; Charest, H.; Barbey, R.; Surdin-Kerjan, Y.
submitted to the EMBL Data Library, December 1993
A;Reference number: S43750
A;Accession: S43750
A:Molecule type: DNA
A;Residues: 1-60, 'I', 62-640 <THO>
A;Cross-references: UNIPARC:UPI00000168CD9; EMBL:L26505; NID:g432493; PID:g432494
C;Genetics:
A;Gene: SGD:MET30
A;Cross-references: SGD:S0001308; MIPS:YIL046w
A;Map position: 9L
F;298-329/Domain: WD repeat homology <WD1>
F;338-369/Domain: WD repeat homology <WD2>
F;374-409/Domain: WD repeat homology <WD3>
F;417-450/Domain: WD repeat homology <WD4>

Query Match 18.7%; Score 538; DB 2; Length 640;
Best Local Similarity 28.4%; Pred. No. 8.9e-33;
Matches 157; Conservative 87; Mismatches 166; Indels 142; Gaps 19;

Qy 62 KRPSGN-----YQEKDL--CIKYFDQWSSDQVEFVHILSRMCHYQHGHINSYLK 112
 Db 117 KRTQEIENIAIKLPLEQSDIHIIISKYSNSNDKIRKLIIDGLISTSCFPQLSYISLVT 176
 Qy 113 PMLQRDITALPEQGLDHAENTLSYLDARSLCAAEVLVCKEWRVISEGMLWKKLIERWV 172
 Db 177 HMIKIDFISLPOE---LSLKLISYLDQSLCNATRVCKRWQKQLADDDRVVHMCQHI 232
 Qy 173 RTDPLWKGLSERR---GWDQYILFKNR-----PTDGPPNSFYRSKY 209
 Db 233 -----DRKPCNGWGLPLLHMKRARIQONSTGSSSNADIQTQTTTPWKVIYERF 282
 Qy 210 PKTIQDIETIESNWRGRHNLQRIQCRSENSK---GVYCLQYDDEKIIISGLRDNISKIW 265
 Db 283 -----KVESNWRKG-----HCRIQEFKGHMDGVLTLQFNRYRLFTGSYDSTIGW 327
 Qy 266 DKTSLECLKVLTGHTGSVLCLOYDERIVITGSSDSTVRVWDVNTGEVLNTLIHHNEAVLH 325
 Db 328 DLFTGKLIRLSGHSQGVKTYLFDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLS 387
 Qy 326 LRFENGLMTVCSKDRSIAVMDMASATDITLRRVLVGHRAAVNVVDFDQKVI--VSASGDR 383
 Db 388 VDSYQKVIIVSGSADKTVKWHVRSCTYLR----GHTEWNCVKLHPKSFSCFCSDDT 443
 Qy 384 TIKWSTSTCEFVRTLNGH---ERGIACLOYRD--RLVWSGSS----- 421
 Db 444 TIRMWDIRTNCLKVFGRHVGQVKIPLTIKOVENLATDNTSDGSSPDQDPTMTDGADE 503
 Qy 422 -----DNTIRLWDIECGACLRVLEGHBEELVRCIRFDNK 454
 Db 504 SDTPSNEQETVLDENIPYPHTLLSCGLDNTIKLWDVKRTGKICRTQFGHVGEVMDIAADNF 563
 Qy 455 RIYSGAYDGKIKWMDLQAALDPRAPASTLCRLTLVEHSGVRFLQDFEQIILSSSHDDTI 514
 Db 564 RIISGSHDGSIKWMDLQ-----SGKCMHTF---NGR--RLQRE-----TQHTQTQ 603
 Qy 515 LIWDFLNVPPSA 526
 Db 604 SIGD--KVAPIA 613

RESULT 6
 T46660
 sulfur controller-2 protein [imported] - Neurospora crassa
 C;Species: Neurospora crassa
 C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
 C;Accession: T46660

```

RESULT 6
T46660
sulfur controller-2 protein [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C/Accession: T46660
R/Kumar, A.; Paietta, J.V.
Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995
A/Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa
A/Reference number: Z23121; MUID:95241499; PMID:7724564
A/Accession: T46660
A/Status: preliminary; translated from GE/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-650 <KUM>
A/Cross-references: UNIPROT:Q01277; UNIPARC:UPI000013566D; EMBL:U17251; NID:980
C/Genetics:
A/Gene: scon-2
A/Map position: 3
A/Introns: 75/3; 319/1; 354/1
C/Function:
A/Description: negatively regulates sulfur structural gene expression
A/Note: scon-2+ expression is dependent on CYS3 function and the binding of CYS3
Query Match 18.2%; Score 525; DB 2; Length 650;
Best Local Similarity 24.2%; Pred. No. 8,7e-32;
Matches 155; Conservative 196; Indels 196; Gaps 16;
Qy 38 CLOSMPSVRCLOISNGTSSVIVSRKRPSEGNVQKEKDLCTIKYFDWSESQVEFVH--- 94
Dh 44 CVYHHPDPSKTERAADRAKRWYMI-----LDKLTSAADO-QAVTHVWS 85

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```
QY 95 -----LISRMCHYQHGHINSYKPMQLORDFITALPEOGLDHAENILSY 138
Db 86 LFSAAPARHRDLMLQGLSCLFPQSFVSVREVNEALKIDFISALPVE-----LAQKVLGY 141
QY 139 LDARSLCAAEALVCKEQRVISEGMLKKLIERMVR---TDPLW-KGLSERRGWDQYLFKN 194
Db 142 LDTVSLTKAAQVSQRWTLADSDAVWVRMCEQHVNRKCTKCGWGLPLERKKLRNRYTRQ 201
QY 195 RPTDGP-----NSFYRL-----YP 210
Db 202 QLAQGGPQVRTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQCAAAEASKAVTQP 261
QY 211 K-----IIQDIETIESNWRGRHNLQRIQCRSENSGVYCLQYDDEKIIISGLRDSIKI 264
Db 262 KTRSWKAVYDRWQVSYNWKNSRYKSLVK-----GHENGVTCLQDDNILATGSYDTTIKI 318
QY 265 WDKTSLECLKVLTHGTSVLCQYDERVIVTGSSDSVTRVMDVNTGVBLNTHLHNEAVL 324
Db 319 WNETECIRTLVGHGTAGIALQFDSDSKLISGLDHTIKVWNWHTGECSTFAAHTDSVI 378
QY 325 HLRFSNGLMVTCKSDRSIAVMDMASATDITLRRVLVGHRAAVNV--VDFDKYIVSASGD 382
Db 379 SVHFDGHLASGSSDKTKVIFDFNSKETCYLK---GHSWVNSTHVDIKSRTVFSASDD 434
QY 383 RTIKWSTSTCEVFTLNHGKRG-----ACIQYRDLVVS-----418
Db 435 TTIKLWLDTRQVIRTYEGHVHVVQVLLPPEYEPDEVLNGASQDNQDAMSVSQSGG 494
QY 419 -----G 419
Db 495 SPSNSHAQIERAGSPGSHSSHNLLPSSLPSGDEVDVRLYGSFAVDESRLPRPYFTWG 554
QY 420 SSDNTIRLWDIEGACLRVLEHGBELVRCIRFDNKRIVSGAYDGKIKVMDLQALDPRAP 479
Db 555 GLDSTMELWDSATGRCLRTLFGHLEGVWSLAGDTIRVISGANDGMVKTWE-----P 605
QY 480 ASTLCLETLVHSGRFRLOQDFEQIISSSHDDTILWDF 519
Db 606 RSGKCDATYTHGCGPFCVGLSLSMASGSEDDGTRLHSF 645

RESULT 7
S62507
hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 05-Oct-2004
C:Accession: T38502; S62507
R:Jones, L.; Murphy, L.; McNeil, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21798
A:Accession: T38502
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-267 <J02>
A:Cross-references: UNIPARC:UPI0000169029; EMBL:Z66525; NID:g1044926; PIDN:CAA91423.1; F
C:Genetics:
F:18-51/Domain: WD repeat homology <WD1>
F:104-137/Domain: WD repeat homology <WD2>

Query Match 17.9%; Score 516.5; DB 2; Length 267;
Best Local Similarity 38.7%; Pred. No. 1.1e-31;
Matches 106; Conservative 54; Mismatches 85; Indels 29; Gaps 6;

QY 259 DNSIKIWDKTSLECLKVLTHGTSVLCQYDER--VIVTGSSDSVTRVMDVNTGEVNTL 316
Db 1 DRTVSDVDSNRFTLYKLYGHSGSVLCDFCRRNLLVSGSSDTIILWQNRPLKVI 60
QY 317 IHNEAVLHFRFNSGLMVTCKSDRSIAVW--DMASATDITLRRVLVGHRAAVNVVDFDK 374
Db 61 FGHTDNVLGVVSVSENYIISRRDHTARVWRDLDTSPAECM-HVLRGHLASVNSVQYSSK 119
QY 375 --YIVASGDRTIKVWSTSTCEVFTLNHGKRGIACTIQLYRDLVSVSGSSDNTIRLWDIEC 432
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```
Db 120 TGLIVTASDRTLRTWDTTGHCIIRIIHAHORGIACAQNGKFIVSGSSDLTIRIPEASS 179
QY 433 GACLRVLEHGBELVRCIRFDNKRIVSGAYDGKIKVMDLQALDPRAPASTLCRLTVEH- 491
Db 180 GKLLRMLQGHEDLIRTVRFNDEKIVSGYDGTVRIN-----FNTGEOHC 224
QY 492 -----SGRFRLOQDFEQIISSSHDDTILWDF 519
Db 225 VLHNSRNSRVLGQDFHRRRIIACHTSHSEILWNF 258

RESULT 8
T22703
hypothetical protein F55B12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22703
R:Simmons, M.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19602
A:Accession: T22703
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-579 <W1>
A:Cross-references: UNIPROT:Q93794; UNIPARC:UPI0000135742; EMBL:Z79757; PIDN:CAB02129.1;
A:Experimental source: clone F55B12
C:Genetics:
A:Gene: CBSP:F55B12.3
A:Map position: 5
A:Introns: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1

Query Match 17.8%; Score 512; DB 2; Length 579;
Best Local Similarity 27.5%; Pred. No. 7.2e-31;
Matches 146; Conservative 77; Mismatches 206; Indels 102; Gaps 15;

QY 51 SNGTSSVIVSRKRPSEGNVQKEKDL-----CIKYFQWSESQDVEFEV 94
Db 31 SNGSSSYNADKLSSSRPLQHKLDLSASPSRNDLNPVREHLIALFKDLSAEQMDAFTR 90
QY 95 LISRMCHYQHGHINSYKPMQLORDFITALPEOGLDHAENILSYLDARSICAAELVCKEW 154
Db 91 LLQESNWNTRIQRLAIEPHFQDFLCLPVE---LGMKILHNLTYDYLKVAQVSKNW 146
QY 155 QRVISSEGMLWKKLIERMVRTDPLWKLSEKRGWDQYLFKNRPTDGPNSF-----204
Db 147 -KLISE-----IDKIWKS-----GVEEFKHPDPTDRTVGTGWTGTAAGVT 188
QY 205 -----YRSLVPKIIQDI-----ETIESNWRRCGRHNLQRIQ---C 235
Db 189 IPDHIQPCDLNVHFRFLKQFGDI FERAADKSYRLRADKIEKNW-----NANPIMGSV 243
QY 236 RSENSKGVYCLQYDDEKIIISGLRDSIKIWDKTSLECLKVLTHGTSVLCQYDE--RVI 293
Db 244 RGHEHDVITCMQIHDDVLVTGSDNTLKWICDKGEVMYTLVGHGTGWTGWTGTAAGVT 303
QY 294 VTGSSDSVTRVMDVNTGEVNTLHNEAVLHFRFNSGLMVTCKSDRSIAVMDMASATDI 353
Db 304 VSGSDTRTVKWSVTVDGSLSLHTLQGHSTVTRCMAMAGSILVTSRDTTLRVDVSGRHL 363
QY 354 TLRRVLVGHRAAVNVVDFDKYIVSASGDRRTIKVWSTSTCEVFTLNHGKRGIACTIQLY 413
Db 364 A---TLHGHHAAVRCVQFDGTTVVSQYDFTVKIWNHTGRCITLTGHNNRVVSLAFES 420
QY 414 R--LVVSGSSDNTIRLWDI---ECGACLRVLEHGBELVRCIRFDNKRIVSGAYDGKIKVW 468
Db 421 ERSIVCSGLSDTSIRVWDFTRPEQECVALLQGHSTLTSGMQLRGNILVSCNADSHVRVW 480
QY 469 DLQALDPRAPASTLCRLTVEHSGRFRLOQ--PDEFOIISSSHDDTILWDF 518
Db 481 DIHEG-----TCVHMLSGHRSATTSLOWFGRNMVATSSDDGTVKLMD 522
```


R;Wolf, D.A.; Jackson, P.K.
Submitted to the EMBL Data Library, December 1997
A:Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in th
A:Reference number: Z22576
A:Accession: T43557
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-703 <WOL>
A:Cross-references: UNIPROT:O14170; UNIPARC:UPI0000131F36; EMBL:AF038867; PIDN:AAB95480.
A:Experimental source: strain h- 972
R;Gentles, S.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1996
A:Reference number: Z21812
A:Accession: T38794
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-703 <GEN>
A:Cross-references: UNIPARC:UPI0000131F36; EMBL:Z98602; PIDN:CAB11275.1; GSPDB:GN000066;
A:Experimental source: strain 972h-; cosmid c4D7
R;Jallepalli, P.V.; Tien, D.; Kelly, T.J.
Proc. Natl. Acad. Sci. U.S.A. 95, 8159-8164, 1998
A:Title: Sud1+ targets' cyclin-dependent kinase-phosphorylated Cdc18 and Rum1 proteins fo
A:Reference number: Z22686; MUID:9818628; PMID:9653157
A:Accession: T43798
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-703 <JAL>
A:Cross-references: UNIPARC:UPI0000131F36; EMBL:AF064515; MID:g3293382; PIDN:AAC39496.1;
C:Genetics:
A:Gene: pop2; sud1; SPAC4D7.03
A:Map position: 1
C:Function:
A:Description: required to prevent spontaneous re-replication

Query Match 13.5%; Score 389.5; DB 2; Length 703;
Best Local Similarity 23.3%; Pred. No. 1.8e-21;
Matches 143; Conservative 113; Mismatches 232; Indels 127; Gaps 25;
QY 3 PDSVIEDKTIELMCSVPRLWGLCANLVESMCAL--SCLOSPSVRCLOISNCTSS-----56
DB 114 PDSVPGDFSISL---VPG-----RNFLYSHSLPPIKTIISDRNNRIKLDNISNSDNF 164
QY 57 ---VIVSRKRPSEGNQYQEKDL-----CIKYFDQWSESDQVEFVEHLISRMCHYQHG 105
DB 165 PPSPKVDSTNTVSPGSKPISEDELDNLQSIQVOTEDIPGQ--SYAFQLLRSNCRQSM 223
QY 106 H-INSYLPMLQDFITAPLPEGLDHIHAIENILSYLDARSLCAAEVLCKEWQVRS-EGWL 163
DB 224 RLLNECEPLKKDILSNLPFS---IVQSILLNLDIHSFLSCLVSPPTWNRILDVHTSY 279
QY 164 WKLLIE---RMVRTDPLWGLSERRGWDQYLFKRPTDGP--PNSFYRS-----LYPK 211
DB 280 WKHMFSLFGQINEND--WKYANPNLNRPPFLHNDQISDDYEPFIFKRHFLNRKWLFPFS 337
QY 212 IIQD-----IETIENWRCGRHNLQR---IQCRSENSK-GVYCL 246
DB 338 IPPSHLSPIHPVNFMTISLLHKDRIITSSGCIQIHNAITGVLEARLEGKEGVAV 397
QY 247 QYDDEKIISGLRDSIKIWDKTSLECLKVLGTGTSVLCQY-----DE 290
DB 398 KIHENTLVSGSIDKTVRVWNIEKAKCTHIFRGHISIIRCLTEILVPSRLIRHGVEIPEPQ 457
QY 291 RVIVTGSSTSVRVWDV-----NTGBV-----LNTLIHNEAVLHLRFSN 330
DB 458 PYIVSGSRDHLRVWKLPRKNTDPPYLPDNTNSIDRWKNPYFVHTLIGHTDSVRTISGV 517
QY 331 GLMVTCSKDRSTAVDMASATDILRRVLVGHRAAVNVVDPDK--YIVSASGDRITIKW 388
DB 518 DLLVSGSDSSIRIRVSTGECYHLR---GHSRLIYSLVYPERNICISGSMKSIKRW 574
QY 389 ---STCTCFVRLTNGHKGKGIACLOYRDLRVVSGSDNTIRLWDIECGACLRVLEGHEELV 446
DB 575 DLSTGCTCKYV--LEGHDAFVTLNLFVQNRLISSADSTIRIWDNTGKPLMVLPSNSGYI 632

QY 447 RCIRFDNKRIVSGAYDGIKIVMDLOALDPRAPASTLCRLTIVHSGRVFRLOQDFEQII 506
DB 633 SSFVSDHEKIIISG-NDGSKVLDWVETG-----KLLRFLTLDTLTKIWHVDFDAMRCV 682
QY 507 SSSHDDTTILWDFLN 521
DB 683 AAVQRDDQAYLEVIN 697
RESULT 14
A:12493
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A12493
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1189 <KUR>
A:Cross-references: UNIPROT:O8YL09; UNIPARC:UPI00000CEEDC; GB:BA000020; PIDN:BA078213.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7129
A:Genome: plasmid

Query Match 13.5%; Score 387.5; DB 2; Length 1189;
Best Local Similarity 28.4%; Pred. No. 5.3e-21;
Matches 91; Conservative 66; Mismatches 112; Indels 51; Gaps 9;
QY 250 DEKIISGLRDSIKIWDKTSLECLKVLGTGTSVLCQYDER--VIVTGSSTSVRVWDV 307
DB 784 DNLILLSGYDSQVKVMDRKTGCLDTLAKKHTNRISVAFHPQGHFLFVSGDDHAAKIWEI 843
QY 308 NTGEVLNLIHNEAVLHL--RFSNGLMVTCSKDRSIAVDM-----ASATDITLRRVL 359
DB 844 GTGQCIKTFQHSNATYTAHNWEHSLASGHEDQTIKLWDLNLSHPKSNVNTHPFRIL 903
QY 360 VGHRAAVNVDFDD--KYIVSASGDRITIKVWSTSCFVRTLNHGRKGTACIQR--DRL 415
DB 904 QGHSNRVSVFVSTGQLLASGADRTIKLWSPHTGQCLHTLHGHSWWAIFSLDDKL 963
QY 416 VVSGSDNTIRLWDIECGACLRVLEGHEELVRCIRF--DNKRIVSGAYDGIKIVWDLO-- 471
DB 964 LASGYDHTVKIWDVSSGQCLQTLQGHGPGSVLAVAFSCDGKTLFSSGYEKLKQWDEVTG 1023
QY 472 -----AALDPRAPAS-----TLCLRTLVEHSGRVFRLOQ 500
DB 1024 YCLOTWEADSNRVAVAVSRDQVLTATGDDSVRLWLDIGKGVCTVTFSGHTSQVICILF 1083
QY 501 --DEPQIISSHDDTILWID 518
DB 1084 TKDGRRMISSSDRTIKIWN 1103

RESULT 15
A:1842
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A1842
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AC1842
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1747 <KUR>
A;Cross-references: UNIPROT:Q8Z020; UNIPARC:UPI000000CDCC1; CB:BA000019; PIDN:BAB77807.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0283

Query Match	13.3%	Score 383.5;	DB 2;	Length 1747;
Best Local Similarity	33.5%	Pred. No. 1.8e-20;		
Matches	85;	Conservative	51;	Mismatches 99;
			Indels	19;
			Gaps	8;

Qy	229	NLQRIQCRSEKGVYCLQY--DDEKIISGLRDNISIKWDKTSLECLKVLTGHTGSLVCL	286
Db	1468	SLSTIQ---KNQNIITTVSYSPDGKTIATASADNTIKLWDSQTOQLIKTLTGHKDRITTL	1524
Qy	287	QY--DERVIVTGSDDSTVRVMDVNTGEVLAHTLIHNEAVLHLRF--NGLMVTCSKDRSI	342
Db	1525	SFHPDNQTIASGSADKTIKIWRVNDGQLRLTLTGHNDVTSVNFSPDGQFLASGSTDNTV	1584
Qy	343	AVMDMASATDITLRRVLVGHRAAVNVYDF--DDKYIVSASGDRTIKVMSTSTCEFVRLN	400
Db	1585	KIWQ----TDGRLIKNTGHGLAIASVKFSPDSHTLASASWDNTIKLWQVTDGKLINLN	1640
Qy	401	GHKRGIAQLQYR--DRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF--DNKRI	456
Db	1641	GHIDGVTSLSFSPDGEILASGSADNTIKLWLPNATLLKTLGLHPGKINTLAFSPDGKTL	1700
Qy	457	VSGAYDGKIKYVDL	470
Db	1701	LSGGEDAGVWVWNL	1714

Search completed: August 25, 2006, 07:23:15
Job time : 44 secs

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation. May
 CC participate in wnt signaling.
 CC -1- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex.
 CC -1- SUBCELLULAR LOCATION: Cytoplasm (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=C;
 CC IsoId=Q9UKB1-1; Sequence=displayed;
 CC Name=A;
 CC IsoId=Q9UKB1-2; Sequence=VSP_006765;
 CC Name=B;
 CC IsoId=Q9UKB1-3; Sequence=VSP_006766;
 CC -1- SIMILARITY: Contains 1 F-box domain.
 CC -1- SIMILARITY: Contains 7 WD repeats.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR ENBL; AF176022; AAF04528.1; -; mRNA.
 DR ENBL; AB033279; BAA92329.1; -; mRNA.
 DR ENBL; AB033280; BAA92330.1; -; mRNA.
 DR ENBL; AB033281; BAA92331.1; -; mRNA.
 DR ENBL; AB014596; BAA31671.1; ALT INIT; mRNA.
 DR ENBL; BC026213; AAH26213.1; -; mRNA.
 DR HSP; Q9Y297; IP22.
 DR Ensembl; ENSG00000072803; Homo sapiens.
 DR H-InVDB; HIX0005413; -.
 DR HGNC; HGNC:13607; FBXW11.
 DR MIM; 605651; Gene.
 DR LinkHub; Q9UKB1; -.
 DR GO; GO:0000151; C:ubiquitin ligase complex; NAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; NAS.
 DR GO; GO:0016567; P:protein ubiquitination; NAS.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS00082; WD_REPEATS_2; 7.
 DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
 DR Alternative splicing; Repeat; Ubl conjugation pathway; WD repeat;
 KW Wnt signaling pathway.
 CHAIN 1 542 F-box/WD-repeat protein 11.
 FT FTId=PRO_0000050981.
 FT DOMAIN 129 167 F-box.
 FT REPEAT 238 275 WD 1.
 FT REPEAT 278 315 WD 2.
 FT REPEAT 318 355 WD 3.
 FT REPEAT 361 398 WD 4.
 FT REPEAT 401 440 WD 5.
 FT REPEAT 442 478 WD 6.
 FT REPEAT 490 527 WD 7.
 FT VARSPLIC 16 49 Missing (in isoform A).
 FT FTId=VSP_006765.
 FT VARSPLIC 16 48 CSVPSRLWLGANLVESMCALSCIQSMPSVRLC -> NTSV

FT MEDONEDESPKNTLW (in isoform B).
 FT /FTId=VSP_006766.
 SQ SEQUENCE 542 AA; 62091 MW; 7CD40087EFAA5C8A CRC64;
 Query Match 100.0%; Score 2879; DB 1; Length 542;
 Best Local Similarity 100.0%; Pred. No. 8.3e-205;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPDSVIEDKTIELMCSVPSRLWLGANLVESMCALSCIQSMPSVRLCQISNGTSSVIVS 60
 DB |||||
 QY 61 RRPSPGNYQKEKDLCKIKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYLKPEMLORDFI 120
 DB |||||
 QY 61 RRPSPGNYQKEKDLCKIKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYLKPEMLORDFI 120
 DB |||||
 QY 121 TALPEQGLDHIABENILSYLDARSLCAELVCKEWQRVISEGMLWKKLIERMVMTDPLWKG 180
 DB |||||
 QY 121 TALPEQGLDHIABENILSYLDARSLCAELVCKEWQRVISEGMLWKKLIERMVMTDPLWKG 180
 DB |||||
 QY 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRGCRHNLQRIQCRSENS 240
 DB |||||
 QY 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRGCRHNLQRIQCRSENS 240
 DB |||||
 QY 241 KGVYCLQYDDEKIIISGLRDNISIKWDKTSLECLKVLGTGTSVLCIQYDERVIVTSSDS 300
 DB |||||
 QY 241 KGVYCLQYDDEKIIISGLRDNISIKWDKTSLECLKVLGTGTSVLCIQYDERVIVTSSDS 300
 DB |||||
 QY 301 TVRVMDVTGCVLNTLIHNEAVLHFRSNGMLVMTCSKORSIAVDMASATDITLRRVLV 360
 DB |||||
 QY 301 TVRVMDVTGCVLNTLIHNEAVLHFRSNGMLVMTCSKORSIAVDMASATDITLRRVLV 360
 DB |||||
 QY 361 GHRAAVNVVDFDDKYIVSAGDRTIKVSTSTCFVTLNGHKGACLOYRDLVVSGS 420
 DB |||||
 QY 361 GHRAAVNVVDFDDKYIVSAGDRTIKVSTSTCFVTLNGHKGACLOYRDLVVSGS 420
 DB |||||
 QY 421 SDNTIRLWDIECGACLVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
 DB |||||
 QY 421 SDNTIRLWDIECGACLVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
 DB |||||
 QY 481 STLCLRLTLVEHSGRVFRLOFDEFQIISSSHDDTLIWDFLNPPSAQNETRSPRTYTI 540
 DB |||||
 QY 481 STLCLRLTLVEHSGRVFRLOFDEFQIISSSHDDTLIWDFLNPPSAQNETRSPRTYTI 540
 DB |||||
 QY 541 SR 542
 DB ||
 QY 541 SR 542
 DB ||
 RESULT 2
 Q5SRV7_MOUSE PRELIMINARY; PRT; 542 AA.
 ID Q5SRV7_MOUSE AC Q5SRV7;
 DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 21-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE F-box and WD-40 domain protein 1B (2 days neonate sympathetic ganglion
 DE cDNA, RIKEN full-length enriched library, clone:7120487019 product:F-
 DE box and WD-40 domain protein 1B, full insert sequence).
 GN Name=Fbxw1b; ORFNames=RP23-94F11.1-002;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hopkins B.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Phillimore B.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."; (4)
 RL Methods Enzymol. 303:19-44(1999).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC PubMed=16141072; DOI=10.1126/science.1112014;
 RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalis V., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano A., Butler B.D., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukehima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Humineck I., Iacono M., Ikeo K., Iwano A., Ishikawa H., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J.P., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Suglura K., Sultana R., Takenaka Y., Taki K., Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamani H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fuka J., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kohjiya M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
 RL Science 309:1559-1563(2005).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RX RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
 RL Science 309:1564-1566(2005).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=22354683; PubMed=12466951; DOI=10.1038/nature01266;
 RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragoti T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kana A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada M., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Yamanaka I., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
 RL Nature 420:563-573(2002).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T., Blake J., Boffelli D., Furuno M., Aono H., Balderelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 RL Nature 409:685-690(2001).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 RL Genome Res. 10:1617-1630(2000).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
 RL Genome Res. 10:1757-1771(2000).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,

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RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AL669951; CA126097.1; -; Genomic DNA.
DR EMBL; AL669844; CA126097.1; JOINED; Genomic DNA.
DR EMBL; AL669844; CA125520.1; -; Genomic DNA.
DR EMBL; AL669951; CA125520.1; JOINED; Genomic DNA.
DR EMBL; AK149139; BA228749.1; -; mRNA.
DR Ensemble; ENSMUSG0000020271; Mus musculus.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GROTEINERPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS00082; WD_REPEATS_2; 7.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Repeat; Ub1 conjugation pathway; WD repeat.
SQ SEQUENCE 542 AA; 62063 MW; D95A78A6977B828A CRC64;

Query Match 99.8%; Score 2872; DB 2; Length 542;
Best Local Similarity 99.6%; Pred. No. 2.8e-204;
Matches 540; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPDSVIEDKTIELMCSVPRSLMGLCANLVESMCALSCLOSMPSVRCQLISNGTSSVIVS 60
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Db 61 RKPSEGNQKEDLCIKYFDQWSESDQVFVEHLISRMCHYQHGHINSYKPMQLQDFI 120
Qy 121 TALPEGLDHAENILSYLDARSICAAELCKEQRVISEGMLWKLIERWRTDPLWKG 180
Db 121 TALPEGLDHAENILSYLDARSICAAELCKEQRVISEGMLWKLIERWRTDPLWKG 180
Qy 181 LSERRGWDQVLFKNRPTDGGPNFYSRLPKIIDIETIESNRCGRHNLQIQRSNS 240
Db 181 LSERRGWDQVLFKNRPTDGGPNFYSRLPKIIDIETIESNRCGRHNLQIQRSNS 240
Qy 241 KGVYCLQYDDEKIISGLRDSIKIWDKTSLECLKVLGTGTSVLCLOYDERVIVTSSDS 300
Db 241 KGVYCLQYDDEKIISGLRDSIKIWDKTSLECLKVLGTGTSVLCLOYDERVIVTSSDS 300
Qy 301 TVRVWDVNTGEVLNLTLIHNEAVLHFRSGLMVTCSKDRSIAVWDMASATDITLRLV 360
Db 301 TVRVWDVNTGEVLNLTLIHNEAVLHFRSGLMVTCSKDRSIAVWDMASATDITLRLV 360
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Qy 481 STLCLRLTLVHSGRVFRLQDFEFOIISSSHDDTLIWDLFNPPSAQNETRSPRTTYI 540
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541 SR 542
541 SR 542

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RESULT 3
Q8K022 MOUSE PRELIMINARY; PRT; 563 AA.
AC Q8K022;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE F-box and WD-40 domain protein 11.
GN Name=Fbxw11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC034261; AAH34261.1; -; mRNA.
DR HSSP; Q9Y297; 1P22.
DR Ensemble; ENSMUSG0000020271; Mus musculus.
DR MGI; MGI:2144023; Fbxw11.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GROTEINERPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS00082; WD_REPEATS_2; 7.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Repeat; Ub1 conjugation pathway; WD repeat.
SQ SEQUENCE 563 AA; 64481 MW; 74D07E6B850ABED CRC64;

Query Match 99.0%; Score 2851.5; DB 2; Length 563;
Best Local Similarity 95.9%; Pred. No. 9.8e-203;
Matches 540; Conservative 2; Mismatches 0; Indels 21; Gaps 1;

Qy 1 MEPDSVIEDKTIELMCSVPRSLMGLCANLVESMCALSCLOSMPSVRCQLISNGTSSVIVS 48

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Db 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCQLNTSVMEDQNE 60
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Db 61 ESPKKSALWQISNGTSSVIVSRKPSSEGNVQKEDLCIKYFDOWSESQVDFVEHLISRM 120
QY 100 CHYQGHINSYKPKMLQDFITALPEQGLDHIENILSYLDARSICAAELVCKEWQVVIS 159
Db 121 CHYQGHINSYKPKMLQDFITALPEQGLDHIENILSYLDARSICAAELVCKEWQVVIS 180
QY 160 EGMWLKLIERWVRTDPLWKLGSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETI 219
Db 181 EGMWLKLIERWVRTDPLWKLGSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETI 240
QY 220 ESNWRCGRHNLQIQRSENSGVYCLQYDDKIISGLRDNSIKIWDKTSLECLKVLGTH 279
Db 241 ESNWRCGRHNLQIQRSENSGVYCLQYDDKIISGLRDNSIKIWDKTSLECLKVLGTH 300
QY 280 TGSVLCLQYDERVIVTGSSTSVRVWVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKD 339
Db 301 TGSVLCLQYDERVIVTGSSTSVRVWVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKD 360
QY 340 RSIADVMDASATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEFVRTL 399
Db 361 RSIADVMDASATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEFVRTL 420
QY 400 NGHKGIAQLOVRDLVVGSSDNTIRLWDIECGACLRVLEGHELVRCIRFDNKRIVSG 459
Db 421 NGHKGIAQLOVRDLVVGSSDNTIRLWDIECGACLRVLEGHELVRCIRFDNKRIVSG 480
QY 460 AYDGKIKVWDIQAALDPRAPASTLCRLTVLHSGRVFRLQDFEQIISSSHDDTLLIWF 519
Db 481 AYDGKIKVWDIQAALDPRAPASTLCRLTVLHSGRVFRLQDFEQIISSSHDDTLLIWF 540
QY 520 LNVPESAQNTRSPRTTYISR 542
Db 541 LNVPESAQNTRSPRTTYISR 563

RESULT 4
Q923H0 MOUSE PRELIMINARY; PRT; 563 AA.
AC Q923H0;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE F-box/WD40 repeat-containing protein HOS.
GN Name=Fbxw1; Synonyms=Fbxw1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN (1) NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N;
RC MEDLINE=21906231; PubMed=11896578; DOI=10.1038/sj.onc.1205311;
RA Bhatia N., Herter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
RT "Mouse homologue of HOS (mHOS) is overexpressed in skin tumors and
RT implicated in constitutive activation of NF-kappaB."
RL Oncogene 21:1501-1509(2002).
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CC -----
CC EMBL: AV038079; AAK72095.1; -; mRNA.
DR HSSP; Q9Y297; 1P22.
DR Ensembl; ENSMUSG00000020271; Mus musculus.
DR MGI; MGI:214023; Fbxw1.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR
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DR Pfam; PF00400; WD40; 7.
DR PRINTS; PRO0320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS0181; FBOX; 1.
DR PROSITE; PS00678; WD REPEATS 1; 5.
DR PROSITE; PS00882; WD REPEATS 2; 7.
DR PROSITE; PS0294; WD REPEATS REGION; 1.
KW Repeat; Ubl conjugation pathway; WD repeat.
SQ SEQUENCE 563 AA; 64742 MW; 9AB562F3FF5E3496 CRC64;

Query Match 95.7%; Score 2755.5; DB 2; Length 563;
Best Local Similarity 93.3%; Pred. No. 1.3e-195;
Matches 525; Conservative 2; Mismatches 15; Indels 21; Gaps 1;

QY 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCI----- 48
Db 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCI----- 60
QY 49 -----QISNGTSSVIVSRKPSSEGNVQKEDLCIKYFDOWSESQVDFVEHLISRM 99
Db 61 ESPKKSALWQISNGTSSVIVSRKPSSEGNVQKEDLCIKYFDOWSESQVDFVEHLISRM 120
QY 100 CHYQGHINSYKPKMLQDFITALPEQGLDHIENILSYLDARSICAAELVCKEWQVVIS 159
Db 121 CHYQGHINSYKPKMLQDFITALPEQGLDHIENILSYLDARSICAAELVCKEWQVVIS 180
QY 160 EGMWLKLIERWVRTDPLWKLGSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETI 219
Db 181 EGMWLKLIERWVRTDPLWKLGSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETI 240
QY 220 ESNWRCGRHNLQIQRSENSGVYCLQYDDKIISGLRDNSIKIWDKTSLECLKVLGTH 279
Db 241 ESNWRCGRHNLQIQRSENSGVYCLQYDDKIISGLRDNSIKIWDKTSLECLKVLGTH 300
QY 280 TGSVLCLQYDERVIVTGSSTSVRVWVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKD 339
Db 301 TGSVLCLQYDERVIVTGSSTSVRVWVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKD 360
QY 340 RSIADVMDASATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEFVRTL 399
Db 361 RSIADVMDAFCHRYHFTPCSGMPRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEFVRTL 420
QY 400 NGHKGIAQLOVRDLVVGSSDNTIRLWDIECGACLRVLEGHELVRCIRFDNKRIVSG 459
Db 421 NGHKGIAQLOVRDLVVGSSDNTIRLWDIECGACLRVLEGHELVRCIRFDNKRIVSG 480
QY 460 AYDGKIKVWDIQAALDPRAPASTLCRLTVLHSGRVFRLQDFEQIISSSHDDTLLIWF 519
Db 481 AYDGKIKVWDIQAALDPRAPASTLCRLTVLHSGRVFRLQDFEQIISSSHDDTLLIWF 540
QY 520 LNVPESAQNTRSPRTTYISR 542
Db 541 LNVPESAQNTRSPRTTYISR 563

RESULT 5
Q8BY90 MOUSE PRELIMINARY; PRT; 529 AA.
AC Q8BY90;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DE 3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE clone:A630019L11 product:F-box/WD-REPEAT PROTEIN 1B (F-BOX AND WD-
DE REPEATS PROTEIN BETA-TRCP2) homolog (F-box and WD-40 domain protein
DE 1B) (Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE clone:I830054B11 product:F-box and WD-40 domain protein 1B, full
DE insert sequence).
GN Name=Fbxw1b; Synonyms=Fbxw1; ORFNames=RP23-94F11.1-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Humaneck I., Iacono M., Ikeo K., Iwano J., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone N., Miyake S., Morris K.,
 RA Mottaqui-Tabar S., Mulder N., Nakano N., Nakaochi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlandi V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Ono Y., Suzuki H., Kawaji J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the mammalian transcriptome.";
 RL Science 309:1564-1566 (2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaio I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawaji J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoh T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio I.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow, and Thymus; STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Iehli Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [19]
RP NUCLEOTIDE SEQUENCE.
RA Phillimore B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE.
RA Hopkins B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [11]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-C57BL/6J; TISSUE=Bone marrow;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AK041532; BAC30975.1; -; mRNA.
DR EMBL; AL669844; CAI25519.1; -; Genomic DNA.
DR EMBL; AL669951; CAI25519.1; JOINED; Genomic DNA.
DR EMBL; AL669951; CAI26098.1; -; Genomic DNA.
DR EMBL; AL669844; CAI26098.1; JOINED; Genomic DNA.
DR EMBL; AK152181; BAE31012.1; -; mRNA.
DR HS3P; Q9Y297; IP22.
DR Ensembl; ENSMUSG00000020271; Mus musculus.

Query Match 92.6%; Score 2665.5; DB 2; Length 529;
Best Local Similarity 92.4%; Pred. No. 5.6e-189;
Matches 512; Conservative 4; Mismatches 1; Indels 37; Gaps 4;

Qy 1 MEPDSVIEDKTIELM-CSV-----PR--SLWLGCANLVESMCALSCQSPSVRL 48
Db 1 MEPDSVIEDKTIELMNTSVMEDQNEDESPKKSALW----- 35

Qy 49 QISNCTSSVIVSRKPSGNYQKEKDLCKYFDQWSESDQVEFVHLLSRMCHYOHGHIN 108
Db 36 QISNCTSSVIVSRKPSGNYQKEKDLCKYFDQWSESDQVEFVHLLSRMCHYOHGHIN 95

Qy 109 SYLKPMQLQDFITALPEQGLDHIAENILSYLDARSALCAELCKEQRVISEGMLWKLI 168
Db 96 SYLKPMQLQDFITALPEQGLDHIAENILSYLDARSALCAELCKEQRVISEGMLWKLI 155

Qy 169 ERWVTDPLWKLSSRRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRH 228
Db 156 ERWVTDPLWKLSSRRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRH 215

Qy 229 NLQIOCSSENSKGVYCLQYDDEKILIGLRNDSIKIMDKTSLECLKVLTGHTGSLCQY 288
Db 216 NLQIOCSSENSKGVYCLQYDDEKILIGLRNDSIKIMDKTSLECLKVLTGHTGSLCQY 275

Qy 289 DERVIVTSSDSTVRVWDVNTGEVLTNLIHNEAVLHFRFNSGLMVTCKORSIAVWDM 348
Db 276 DERVIVTSSDSTVRVWDVNTGEVLTNLIHNEAVLHFRFNSGLMVTCKORSIAVWDM 335

Qy 349 SATDITLRRVLVGHRAAVNVVDFDDKIYVSAGSDRTIKVWSTSTCEFTVTLNGHKGRIAC 408
Db 336 SATDITLRRVLVGHRAAVNVVDFDDKIYVSAGSDRTIKVWSTSTCEFTVTLNGHKGRIAC 395

Qy 409 LQYDRDLVVSGSSDNTIRLWDIEGACLRVLEHGHEELVRCIRFNDKRVISGAYDGKIKW 468
Db 396 LQYDRDLVVSGSSDNTIRLWDIEGACLRVLEHGHEELVRCIRFNDKRVISGAYDGKIKW 455

Qy 469 DLQALDPRAPASTLCRLTLVHSGRVRPRLQFDEFOIISSSHDDTILWDLNVPSPAQN 528
Db 456 DLQALDPRAPASTLCRLTLVHSGRVRPRLQFDEFOIISSSHDDTILWDLNVPSPAQN 515

Qy 529 ETRSPSRITYTYISR 542
Db 516 ETRSPSRITYTYISR 529

RESULT 6
Q3TLZ8_MOUSE
ID Q3TLZ8_MOUSE PRELIMINARY; PRT; 529 AA.
AC Q3TLZ8;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Mammary gland RCB-0526 JyG-MC(A) cDNA, RIKEN full-length enriched
DE library, clone:G830018H24 product:F-box and WD-40 domain protein 1B,
DE full insert sequence.
GN Name=FBXw1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
EX MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic M.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Anweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M.P., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Humanecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
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RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakao H., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiyara K., Sultana R., Takenaka Y., Taki K.,
RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grammond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Walthedst C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,

QY 229 NLORIQRSENSKGVYCLQYDDDEKIISGLRDNISIKIWDKTSLECLKVLTHGHTGSLVCLQY 288
DB 216 NLORIQRSENSKGVYCLQYDDDEKIISGLRDNISIKIWDKTSLECLKVLTHGHTGSLVCLQY 275
QY 289 DERIVITGSSDSTVRVWDVNTGEVLNTLHNEAVLHLRFSNGLMVTCSKORSIAVWDMA 348
DB 276 DERIVITGSSDSTVRVWDVNTGEVLNTLHNEAVLHLRFSNGLMVTCSKORSIAVWDMA 335
QY 349 SATDITLRLVLGHRAAVNVVDFDDKYIVSASGDRITIKWSTSTCEFFVRTLNGHKGRIAC 408
DB 336 SATDITLRLVLGHRAAVNVVDFDDKYIVSASGDRITIKWSTSTCEFFVRTLNGHKGRIAC 395
QY 409 LOYDRVLVVGSSDNTIRLWDIECGACRLVRLEGHEELVRCIRFDNKRIVSGAYDGKIKVW 468
DB 396 LOYDRVLVVGSSDNTIRLWDIECGACRLVRLEGHEELVRCIRFDNKRIVSGAYDGKIKVW 455
QY 469 DLOAALDPRAPASTLCRLTLVHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQN 528
DB 456 DLOAALDPRAPASTLCRLTLVHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQN 515
QY 529 ETRSPSRITYTISR 542
DB 516 ETRSPSRITYTISR 529
RESULT 7
Q3TCM9_MOUSE 4 PRELIMINARY; PRT; 508 AA.
AC Q3TCM9_MOUSE 4 PRELIMINARY; PRT; 508 AA.
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE 17 days embryo kidney cDNA. RIKEN full-length enriched library.
DE clone:1920043C06 product:F-box and WD-40 domain protein 1B, full
DE insert sequence (Osteoclast-like cell cDNA, RIKEN full-length enriched
DE library, clone:1420048G02 product:F-box and WD-40 domain protein 1B,
DE full insert sequence).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RC MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX "High-efficiency full-length cDNA cloning."
RA Carninci P., Hayashizaki Y.;
RL Methods Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RC PubMed=16141072; DOI=10.1126/science.1112014;
RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A.,
RA Bamsel-Implombato A., Bewell R., Bhatnagar R., Bhatnagar R., Bhatnagar R.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Humenicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Larsen L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Fabriz S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,

RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Ouackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome."
RL Science 309:1559-1563(2005).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RC PubMed=16141073; DOI=10.1126/science.1112009;
RX RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome."
RL Science 309:1564-1566(2005).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Ouackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RC MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

HSP: Q9Y297; 1P22.
 DR Ensembl; ENSMUSG00000020271; Mus musculus.
 DR MGI: 2144023; Fbxw11.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS0181; FBOX; 1.
 DR PROSITE; PS00678; WD REPEATS 1; 5.
 DR PROSITE; PS0082; WD REPEATS 2; 7.
 DR PROSITE; PS0294; WD REPEATS_REGION; 1.
 DR WD repeat.
 KW NON TER
 FT SEQUENCE 555 AA; 63288 MW; 6025496DBAC6A489 CRC64;
 Query Match 92.4%; Score 2660; DB 2; Length 555;
 Best Local Similarity 93.4%; Pred. No. 1.5e-188;
 Matches 506; Conservative 2; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MEPDSVIEDKTIELMCSVPSRLWLGANLVESMCALCSQSMPSVRCIQISNGTSSVIVS 60
 DB 48 MEPDSVIEDKTIELM-----ISNGTSSVIVS 73
 QY 61 RKRPSSEGNVQKEDLCIKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYLKPMQORDFI 120
 DB 74 RKRPSSEGNVQKEDLCIKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYLKPMQORDFI 133
 QY 121 TALPEQGLDHAENILSYLDARSLCAELVCKEQRVISEGMLWKKLIERVMVTDPLWKG 180
 DB 134 TALPEQGLDHAENILSYLDARSLCAELVCKEQRVISEGMLWKKLIERVMVTDPLWKG 193
 QY 181 LSEREGWQDYLKFNRPDTGPPNSFYRSLYPKIIQDIETIESNRCGRHNLQIQCRSENS 240
 DB 194 LSEREGWQDYLKFNRPDTGPPNSFYRSLYPKIIQDIETIESNRCGRHNLQIQCRSENS 253
 QY 241 KGVYCLQYDDDKIIISGLRDNSIKIWDKTSLECLKVLGTGHTGSLVCLQYDERVIVTGSSDS 300
 DB 254 KGVYCLQYDDDKIIISGLRDNSIKIWDKTSLECLKVLGTGHTGSLVCLQYDERVIVTGSSDS 313
 QY 301 TVRVMDVNTGEVLTLIHNEAVLHLRFSNGLMVTCSKDRSTAVWDMASATDITLRRVLV 360
 DB 314 TVRVMDVNTGEVLTLIHNEAVLHLRFSNGLMVTCSKDRSTAVWDMASATDITLRRVLV 373
 QY 361 GHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEVFRTLNHKGRIACIQYRDRLVWSGS 420
 DB 374 GHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEVFRTLNHKGRIACIQYRDRLVWSGS 433
 QY 421 SNTIRLWDIECGACLRVLEGEHELVRGIRFNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
 DB 434 SNTIRLWDIECGACLRVLEGEHELVRGIRFNKRIVSGAYDGKIKVWDLQAALDPRAPA 493
 QY 481 STLCLRTLVEHSGRFRLOQDFEQIISSHDDTILIWDFLNPVPSAQNTPSPRTYVI 540
 DB 494 STLCLRTLVEHSGRFRLOQDFEQIISSHDDTILIWDFLNPVPSAQNTPSPRTYVI 553
 QY 541 SR 542
 DB 554 SR 555
 RESULT 9
 Q5ZH09 CHICK
 ID Q5ZH09_CHICK PRELIMINARY; PRT; 529 AA.
 AC Q5ZH09;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DR Hypothetical protein.
 GN ORFNames=RCJMB04_34f17;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CB; TISSUE=Bursa;
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
 RA Fiedler P., Kutter S., Blagodatki A., Kostovska D., Koter M.,
 RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
 RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
 RT gene function analysis.";
 RL Genome Biol. 6:R6-R6(2005).
 CC -----
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 CC -----
 DR EMBL; AJ721075; CAG32734.1; -; mRNA.
 DR GO; GO:0006512; P:ubiquitin cycle; IEA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS0181; FBOX; 1.
 DR PROSITE; PS00678; WD REPEATS 1; 5.
 DR PROSITE; PS0082; WD REPEATS 2; 7.
 DR PROSITE; PS0294; WD REPEATS_REGION; 1.
 DR KW Hypothetical protein; Repeat; Ub1 conjugation pathway; WD repeat.
 DR SEQUENCE 529 AA; 60924 MW; 0DCD9905P5D0F1E7 CRC64;
 Query Match 92.1%; Score 2652.5; DB 2; Length 529;
 Best Local Similarity 91.9%; Pred. No. 5.1e-188;
 Matches 509; Conservative 2; Mismatches 6; Indels 37; Gaps 3;
 QY 1 MEPDSVIEDKTIELM-CSV-----PRLWLGANLVESMCALCSQSMPSVRCVL 48
 DB 1 MEPDSVIEDKTIELMNTSVMEDQNEDESPKNTLM----- 35
 QY 49 QISNGTSSVIVSRKRPSSEGNVQKEDLCIKYFDQWSESDQVEFVEHLISRMCHYOHGHIN 108
 DB 36 QISNGTSSVIVSRKRPSSEGNVQKEDLCIKYFDQWSESDQVEFVEHLISRMCHYOHGHIN 95
 QY 109 SYLKPMQORDFITALPEQGLDHAENILSYLDARSLCAELVCKEQRVISEGMLWKKLI 168
 DB 96 SYLKPMQORDFITALPEQGLDHAENILSYLDARSLCAELVCKEQRVISEGMLWKKLI 155
 QY 169 ERMVTRDPLWKLSERRGWQDYLKFNRPDTGPPNSFYRSLYPKIIQDIETIESNRCGRH 228
 DB 156 ERMVTRDPLWKLSERRGWQDYLKFNRPDTGPPNSFYRSLYPKIIQDIETIESNRCGRH 215
 QY 229 NLQIQCRSENSKGVYCLQYDDEKIIISGLRDNSIKIWDKTSLECLKVLGTGHTGSLVCLQY 288
 DB 216 NLQIQCRSENSKGVYCLQYDDEKIIISGLRDNSIKIWDKTSLECLKVLGTGHTGSLVCLQY 275
 QY 289 DERIVITVGSSTVRVMDVNTGEVLTLIHNEAVLHLRFSNGLMVTCSKDRSIWDMNA 348
 DB 276 DERIVITVGSSTVRVMDVNTGEVLTLIHNEAVLHLRFSNGLMVTCSKDRSIWDMNA 335
 QY 349 SATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEVFRTLNHKGRIAC 408
 DB 336 SPTDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEVFRTLNHKGRIAC 395
 QY 409 LOYRDLRVVSGSSDNTIRLWDIECGACLRVLEGEHELVRGIRFNKRIVSGAYDGKIKVW 468
 DB 396 LOYRDLRVVSGSSDNTIRLWDIECGACLRVLEGEHELVRGIRFNKRIVSGAYDGKIKVW 455
 QY 469 DIQAAALDPRAPASTLCLRTLVEHSGRFRLOQDFEQIISSHDDTILIWDFLNPVPSAQN 528

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Db 456 DLQALDPRAPASTLCRLTLVHSGRVRLQDFEQIISSSHDDTLIWDFLNVPSPAPN 515
Qy 529 ETRSPRTTYISR 542
Db 516 ETRSPRTTYISR 529

RESULT 10
Q6PGW4 BRARE
ID Q6PGW4 BRARE PRELIMINARY; PRT; 527 AA.
AC Q6PGW4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE zgc:63728.
GN ORFNames=zgc:63728;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Haney J., Helton E., Kettelman M., Madan A., Rodriguezes S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.F.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL; BC056809; AAH56809.1; -; mRNA.
DR Ensembl; ENSDARG0000017230; Danio rerio.
DR ZFIN; ZDB-GENE-040426-2903; zgc:63728.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR P-ODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS00082; WD_REPEATS_2; 7.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; Ub1 conjugation pathway; WD repeat.
SQ SEQUENCE 527 AA; 60547 MW; 563F3C014CA099C3 CRC64;
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Query Match 85.0%; Score 2448.5; DB 2; Length 527;
Best Local Similarity 86.1%; Pred. No. 7e-173;
Matches 466; Conservative 30; Mismatches 26; Indels 19; Gaps 4;

Qy 7 IEDKTIELMCSVPRSLWGLCANLVESMCA-----LSCLQSMPSVRCQLQISNGTSSTVIVSR 61
Db 1 MEDKTIQLQNT-----SVMDPQTADRSKPTLIKSS--TFICPQVSNQ--PLTGSR 46

Qy 62 KRPSGNYOKEKDLCTKYFDQWSESQVFEVHILSRMCHYQHGHINSYLNKPLQORDFIT 121
Db 47 KRPSGNYEKEKDVCTQLFDQWSEADQVFEVHILSRMCHYQHGHINSYLNKPLQORDFIT 106

Qy 122 ALPEQGLDHAENILSYLDARSLCAELVCKEQRVISEGMLWKKLIERVVRDPLWKGL 181
Db 107 ALPAQGLDHAENILSYLDARSLCAELVCKEQRVISEGMLWKKLIERVVRDPLWKGL 166

Qy 182 SERRGWDQVLFKNRPTDGPNSFYRLPKIIQDIETIESNMRCGRHNLQRIQCRSENSK 241
Db 167 SERHQWEKYLFKORTTEVPNSFYRLPKIIQDIETIEANWCGRRHNLQRIQCRSENSK 226

Qy 242 GVCYLOYDDEKIIISGLRDNSIKIWDKYSLECLKVLTHGTGSLVLCQYDERVIVTGSSDST 301
Db 227 GVCYLOYDDEKIIISGLRDNSIKIWDKQTLKLTGHTGSLVLCQYDERVIVTGSSDST 286

Qy 302 VRVMDVNTGEVLNTHHNEAVLHFRSNGLMVTCSDKRSIAVMDMASATDITLRRVLVG 361
Db 287 VRVMDVNSGEVLNTHHNEAVLHFRFCNGLMVTCSKDRSIAVMDMASPTDISLRRVLVG 346

Qy 362 HRAAVNVVDFDDKYIVSASGDRTIKWVSTSTCEVFTLNGHKGRIACQYRDRDLVWSSGSS 421
Db 347 HRAAVNVVDFDDKYIVSASGDRTIKWVSTSTCEVFTLNGHKGRIACQYRDRDLVWSSGSS 406

Qy 422 DNTIRLWDEICGACLRVLEGEHELVCIRPDNKRIVSGAYDGIKQVMDLQALDPRAPAS 481
Db 407 DNTIRLWDEICGACLRVLEGEHELVCIRPDNKRIVSGAYDGIKQVMDLQALDPRAPAS 466

Qy 482 TLCRLTLVHSGRVRLQDFEQIISSSHDDTLIWDFLNVPSPAPN 541
Db 467 TLCRLTLVHSGRVRLQDFEQIISSSHDDTLIWDFLNVPSPAPN 526

Qy 542 R 542
Db 527 R 527

RESULT 11
FBW1A HUMAN
ID FBW1A HUMAN STANDARD; PRT; 605 AA.
AC Q9Y297; Q9Y213;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 52.
DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
DE (E3RSIkappa) (pIkappaAlpha-E3 receptor subunit).
GN Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT "Identification of the receptor component of the IkappaAlpha-
RT ubiquitin ligase".
RL Nature 396:590-594 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RC TISSUE=Lymphoid;
RX MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;
RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
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December 10

Thomas D., Strebel K., Benarous R.;
"A novel human WD protein, h-beta TrCP, that interacts with HIV-1 Vpu connects CD4 to the ER degradation pathway through an F-box motif."; Mol. Cell 1:565-574 (1998).
[3]
RN NP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RN RX MEDLINE=2003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2; Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M., Pagano M.;
"Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179 (1999).
[4]
RN NP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RN RC TISSUE=Brain;
RN RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[5]
RN NP CHARACTERIZATION.
RN RX MEDLINE=99145464; PubMed=9990852;
RN RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J., Harper J.W.;
"The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically with phosphorylated destruction motifs in I-kappa-B-alpha and beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro."; Genes Dev. 13:270-283 (1999).
[6]
RN NP INTERACTION WITH UBQLN1.
RN RC TISSUE=B-cell;
RN RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X; Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E., Kedersha N.L., Gill G., Howley P.M.;
"The hPLIC proteins may provide a link between the ubiquitination machinery and the proteasome."; Mol. Cell 6:409-419 (2000).
[7]
RN NP INTERACTION WITH PHOSPHORYLATED CTNNB1.
RN RX MEDLINE=22072105; PubMed=1207367;
RN RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z., Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
"Regulation of S33/S37 phosphorylated beta-catenin in normal and transformed cells."; J. Cell Sci. 115:2771-2780 (2002).
[8]
RN NP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1 AND CTNNB1.
RN RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X; Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W., Pavletich N.P.;
"Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin ligase."; Mol. Cell 11:1445-1456 (2003).
[9]
RN NP FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-box protein) ubiquitin ligase complex, which mediates the

ubiquitination of proteins involved in cell cycle progression, signal transduction and transcription. Regulates the stability of CTNNB1 and participates in Wnt signaling.
-!- PATHWAY: Ubiquitin conjugation; third step.
-!- SUBUNIT: Interacts directly with SKP1 in the SCF complex. Interacts specifically with phosphorylated CTNNB1 and NFKB1A, ubiquitination substrates. Binds UBQLN1.
-!- SUBCELLULAR LOCATION: Cytoplasm.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
Name=2;
IsoId=O9Y297-1; Sequence=Displayed;
Names=2;
IsoId=O9Y297-2; Sequence=VSP_006764;
Names=2;
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 7 WD repeats.
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EMBL: AF101784; AAC08702.1; -; mRNA.
EMBL: Y14153; CAA74572.1; -; mRNA.
EMBL: AF129530; AAF04464.1; -; mRNA.
EMBL: BC027994; AAH27994.1; -; mRNA.
PDB: 1P22; X-ray; A=175-605.
IntAct: O9Y297;
Ensembl: ENSG00000166167; Homo sapiens.
HGNC: HGNC:1144; BTRC.
MIM: 603482; gene.
LinkHub: O9Y297;
GO: GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
GO: GO:007165; P:signal transduction; TAS.
GO: GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
InterPro: IPR001810; F-box.
InterPro: IPR001680; WD40.
Pfam: PF00646; F-box; 1.
PRINTS: PF00400; WD40; 7.
ProDom: PD000018; WD40; 4.
SMART: SM00256; FBOX; 1.
SMART: SM00320; WD40; 7.
PROSITE: PS0181; FBOX; 1.
PROSITE: PS00678; WD_REPEATS_1; 6.
PROSITE: PS0082; WD_REPEATS_2; 7.
PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW 3D-structure; Alternative splicing; Ligase; Polymorphism; Repeat;
KW Ub1 conjugation pathway; WD repeat; Wnt signaling pathway.
CHAIN 1 605 F-box/WD-repeat protein 1A.
FTID=PRO_0000050980.
DOMAIN 190 228 P-box.
REPEAT 301 338 WD 1.
REPEAT 341 378 WD 2.
REPEAT 381 418 WD 3.
REPEAT 424 461 WD 4.
REPEAT 464 503 WD 5.
REPEAT 505 541 WD 6.
REPEAT 553 590 WD 7.
VARSPPLIC 17 52 Missing (in isoform 2).
FTID=VSP_006764.
VARIANT 543 543 A -> S (in dbSNP:4151060).
FTID=VAR_022027.
VARIANT 592 592 P -> H (in dbSNP:2270439).
FTID=VAR_020119.
STRAND 176 176
HELIX 180 183
TURN 184 184
HELIX 185 187
TURN 188 188
HELIX 190 197
TURN 198 199
HELIX 202 211
TURN 213 221
TURN 222 223


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FT HELIX 224 233
FT TURN 234 234
FT STRAND 235 235
FT HELIX 237 244
FT STRAND 245 247
FT HELIX 248 251
FT STRAND 265 265
FT HELIX 266 285
FT TURN 286 288
FT STRAND 296 297
FT STRAND 301 302
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FT STRAND 395 400
FT TURN 401 402
FT STRAND 403 403

Query Match 84.9%; Score 2445.5; DB 1; Length 605;
Best Local Similarity 75.7%; Pred. No. 1.4e-172;
Matches 456; Conservative 49; Mismatches 35; Indels 63; Gaps 4;

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Db 1 MDPAAEVLQEKALFKMCSMPRLWLGCSLADSMPSRLCLYNPGTALTAFQNSSEDEC 60

Qy 40 -----QSMPSVRCL---QISNGTSSVIV 59
Db 61 NNGEPPRKIIPEKNSLRQTYNSCARCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV 120

Qy 60 SRKRPSEGNQYKQKDLCKIKYFDQWSESQDQVEFVHLSIRCHYQHGHINSYLKPMQLQDF 119
Db 121 PKORKLSASVEKEKELCVKYPQEQWSESQDQVEFVHLSIRCHYQHGHINSYLKPMQLQDF 180

Qy 120 ITALPEQGLDHAENILSYLDARSCLCAELVCKEQRVISEGMLWKKLIERMVVRTDPLWK 179
Db 181 ITALPARGLDHAENILSYLDARSCLCAELVCKEQRVISEGMLWKKLIERMVVRTDPLWK 240

Qy 180 GLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPKIIQDIETIESNWRGCRHNLQROCRS 237
Db 241 GLAERRGWQYLFKNRPPDGNAPPNSFYRALYPKIIQDIETIESNWRGCRHSLQRIHCRS 300

Qy 238 ENSGVYVCLOYDDKIIISGLRDSIKTKWDKTSLECLVLTGHTCSVLLOYDERVIVTGS 297
Db 301 ETSKGVYVCLOYDDKIIISGLRDSIKTKWDKTSLECLVLTGHTCSVLLOYDERVIVTGS 360

Qy 298 SDSVTRVWMDVNTGEMLNTLIHNEAVLHRLFRSNGLWVTCSDRSIAVWDMASATDITLRR 357
Db 361 SDSVTRVWMDVNTGEMLNTLIHNEAVLHRLFRSNGLWVTCSDRSIAVWDMASATDITLRR 420

Qy 358 VLVGHRAAVNVDPDDKYIVSASGDRTIKWSTSTCFVFTLNHGKRGIAQLQYRDLVV 417
Db 421 VLVGHRAAVNVDPDDKYIVSASGDRTIKWSTSTCFVFTLNHGKRGIAQLQYRDLVV 480

Qy 418 SGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKKRIVSGAVDGKIKVWDLOAALDPR 477
Db 481 SGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKKRIVSGAVDGKIKVWDLOAALDPR 540

Qy 478 APASTLCLRLTIVHSGRVFRQLQDFEQIISSSHDDTILIWDFLNVPPSAQNETRSPSRTY 537
Db 541 APACTLCLRLTIVHSGRVFRQLQDFEQIIVSSSHDDTILIWDFLNDPAQAEPSPSRTY 600

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Qy 538 TYISR 542
Db 601 TYISR 605

RESULT 12
Q5W141_HUMAN PRELIMINARY; PRT; 605 AA.
ID Q5W141;
AC Q5W141;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-PEB-2006, entry version 11.
DE Beta-transducin repeat containing.
GN Name=BTRC; ORFNames=RP11-529I10.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Whitehead S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bird C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Clark S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AL133387; CAH70020.1; -; Genomic DNA.
DR EMBL; AL445463; CAH70020.1; JOINED; Genomic DNA.
DR EMBL; AL627424; CAH70020.1; JOINED; Genomic DNA.
DR EMBL; AL445463; CAI12963.1; -; Genomic DNA.
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DR EMBL; AL627424; CAI1042.1; -; Genomic DNA.
DR EMBL; AL133387; CAI1042.1; JOINED; Genomic DNA.
DR EMBL; AL445463; CAI1042.1; JOINED; Genomic DNA.
DR EMBL; ENSG00000166167; Homo sapiens.
DR GO; GO:0006512; Pubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS0181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS00882; WD_REPEATS_2; 7.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; Ub1 conjugation pathway; WD repeat.
SQ SEQUENCE 605 AA; 68867 MW; 4C67F3B7E400FD37 CRC64;

Query Match 84.9%; Score 2445.5; DB 2; Length 605;
Best Local Similarity 75.7%; Pred. No. 1.4e-172;
Matches 456; Conservative 49; Mismatches 35; Indels 63; Gaps 4;

Qy 1 MEP-DSVIEDKTIELMCSVPRSLWLCANLVESMCALSCIL----- 39
Db 1 MDPAAEVLQEKALFKMCSMPRLWLGCSLADSMPSRLCLYNPGTALTAFQNSSEDEC 60

Qy 40 -----QSMPSVRCL---QISNGTSSVIV 59
Db 61 NNGEPPRKIIPEKNSLRQTYNSCARCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV 120

Qy 60 SRKRPSEGNQYKQKDLCKIKYFDQWSESQDQVEFVHLSIRCHYQHGHINSYLKPMQLQDF 119

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Qy 120 ITALPEOGLDHAENILSYLDARSILCAELVCKEQRVISEGMLWKKLIERWRTDPLWK 179
Db 181 ITALPARGLDHIAENILSYLDAKSLCAELVCKEQRVITSDGMLWKKLIERWRTDSLWR 240
Qy 180 GLSERRGWDQYLFKNRPTDG--PPNSFVRSYLPKIIQDIETESNWRGCRNLQRIQCRS 237
Db 241 GLAERRGWQYLFKNRPPDGNAPNSFYRALYPKIIQDIETESNWRGCRSLQRIHCRS 300
Qy 238 ENSKGVCYQYDDDEKIIISGLRDNSTIKWDTSLKCLKVLTHGTSVLCQYDDEIVITGS 297
Db 301 ETSKGVCYQYDDQKIVSGLRDNSTIKWDTSLKCLKVLTHGTSVLCQYDDEIVITGS 360
Qy 298 SDSTVRVWVNTGEVNTLIHNEAVLHRSNGLMVTCSKDRSTAVWDMASATDITLRR 357
Db 361 SDSTVRVWVNTGEMNTLIHNEAVLHRSNGLMVTCSKDRSTAVWDMASATDITLRR 420
Qy 358 VLVGHRAAVNVVDFDKYIVSASGDRITIKWSTSTCFVRTLNHKGRIACLOYRDLVV 417
Db 421 VLVGHRAAVNVVDFDKYIVSASGDRITIKWSTSTCFVRTLNHKGRIACLOYRDLVV 480
Qy 418 SGSSDNTIRLWDIEGACLRVLGHEELVRCIRFNDKRVISGAYDGKIKVWDLQALDPR 477
Db 481 SGSSDNTIRLWDIEGACLRVLGHEELVRCIRFNDKRVISGAYDGKIKVWDLVAAALDPR 540
Qy 478 APASTLCURTIVHSGRVRFRLODFQIISSHDDTILWFLNVPVPSAQNSTRSPSRTY 537
Db 541 APAGTLCURTIVHSGRVRFRLODFQIIVSSSHDDTILWFLNVPVPSAQNSTRSPSRTY 600
Qy 538 TYISR 542
Db 601 TYISR 605

RESULT 13
ID Q3UL2_MOUSE PRELIMINARY; PRT; 605 AA.
AC Q3UL2_MOUSE
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Blastocyst blastocyst cDNA, RIKEN full-length enriched library,
DE clone:1C002312 product:beta-transducin repeat containing protein,
DE full insert sequence.
GN Name=Btrc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,

Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Huminek L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
Kicano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
Mortagui-Tabar S., Mulder N., Nakano N., Nakautchi H., Ng P.,
Nielsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
Roat B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
Kawashima T., Kojima M., Kondo S., Konno K., Nakano K., Ninomiya N.,
Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome."
RL Science 309:1559-1563(2005).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome."
RL Science 309:1564-1566(2005).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Pavasoti N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kogawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hata A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio J.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts N.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20495374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa K., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa K., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanegawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: AK145624; BAB26547.1; -; mRNA.
 DR MGI: MGI1339871; Btrc.
 DR GO: GO:0005783; C:endoplasmic reticulum; RCA.
 DR GO: GO:0004840; F:ubiquitin conjugating enzyme activity; RCA.
 DR GO: GO:0006464; P:protein modification; RCA.
 DR GO: GO:0007165; P:signal transduction; RCA.
 DR GO: GO:0006511; P:ubiquitin-dependent protein catabolism; RCA.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.

DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS0082; WD_REPEATS_2; 7.
 DR PROSITE; PS0094; WD_REPEATS_REGION; 1.
 KW Repeat; Ubl conjugation pathway; WD repeat.
 SQ SEQUENCE 605 AA; 68942 MW; 557B3942F52DC472 CRC64;
 Query Match 84.7%; Score 2437.5; DB 2; Length 605;
 Best Local Similarity 75.4%; Pred. No. 5.5e-172;
 Matches 456; Conservative 51; Mismatches 35; Indels 63; Gaps 4;
 QY 1 MEP-DSVIEDKTIELMCSVPRSLWLGLCANLVSFMCALSC-----QSMPSVRL---QISNGTSSVIV 39
 DB 1 MDPAAEVLQEKALKFMCSPRSLWLGLCCSLADSMPSRLCLYNPGLTALFQNSRREDC 60
 QY 40 -----QSMPSVRL---QISNGTSSVIV 59
 DB 61 NNGEPPRKIIPEKNSLRQTYNSCARLCINQETVCLTSTAMKTENCVAKAKLANGTSSMIV 120
 QY 60 SRKRPSEGNVYQEKDLCIKYFQWSESQDOVEFVEHLISRMCHYOHGHINSYKPMLODF 119
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 QY 120 ITALPEQGLDHAENILSYLDARSLCAELVCKEWMORVISEGMLWKKLIERMVVRTDPLWK 179
 DB 181 ITALPARGLDHAENILSYLDARSLCAELVCKEWMORVISEGMLWKKLIERMVVRTDPLWK 240
 QY 180 GLSERGWDQYLFKNRPTD--GPPNSFYRSLYPKIIQDIETIESNWRCCGRHNIQRIQCRS 237
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 QY 298 SOSTVVRVDVNTGVLNTLIHNEAVLHURFNSGLMVTCKDSRIAVWDMASATDITLRR 357
 DB 361 SOSTVVRVDVNTGVLNTLIHNEAVLHURFNSGLMVTCKDSRIAVWDMASATDITLRR 420
 QY 358 VLVGHRAAVNVVDFDDKYIVSASGDRITIKVMTSTCEPVRTLNHGRKGIACLYRDLVV 417
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 QY 418 SGSSDNTIRLWDIECGACLRVLEEGHEELVRCIRFDNKRIVSGAYDGGIKVWDLQALDPR 477
 DB 481 SGSSDNTIRLWDIECGACLRVLEEGHEELVRCIRFDNKRIVSGAYDGGIKVWDLQALDPR 540
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 DB 541 APAGTLCRLTLVHSGRVFRLOQDFEQIISSSHDDTLILWDFLNVPPSAQNETRSPSRTY 600
 QY 538 TYISR 542
 DB 601 TYISR 605
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 AC Q571K6;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DE MKIAA4123 protein (Fragment).
 GN Name=Btrc; Synonyms=mkIAA4123;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;

RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RT Saga Y., Nagase T., Ohata O., Koga H.;
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
 RT The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
 RT Identified by Screening of Terminal sequences of cDNA Clones Randomly
 RT Sampled from Size-Fractionated Libraries.,"
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AK220183; BAD90368.1; -; mRNA.
 DR Ensembl; ENSMUSG00000025217; Mus musculus.
 DR MGI; MGI:1338871; Btrc.
 DR GO; GO:0005783; C:endoplasmic reticulum; RCA.
 DR GO; GO:0004840; E:ubiquitin conjugating enzyme activity; RCA.
 DR GO; GO:0006464; P:protein modification; RCA.
 DR GO; GO:0007165; P:signal transduction; RCA.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; RCA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
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 DR PROSITE; PS00678; WD_REPEATS_1; 6.
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 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW WD repeat.
 FT NON TER
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 Query Match 84.6%; Score 2436.5; DB 2; Length 639;
 Best Local Similarity 75.4%; Pred. No. 7e-172;
 Matches 456; Conservative 50; Mismatches 36; Indels 63; Gaps 4;
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 DB 95 NNGEPKRIIPKNSLRQYNSCARCLINQETVCLTSTAMKTCNCVAKLANGTSSIV 154
 QY 60 SRKRPSEGNQKEKDLCTKYFDQWSESQVEFVEHLISRMCHYQHGHSYLYKPLQDRP 119
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 DB 215 ITALPARGLDHTAENILSYLDARSLCAAELVCKEWRVYVTSQGLWKKLIERMVTDLSLR 274
 QY 180 GLISRRGWQDLFKNRPTD--GPPNSFYRSYLPKIIQDIETTESNWRGCRNLQRIQCRS 237
 DB 275 GLAERGHGQYLFKNKPPDENAPPNSFYRSLYLPKIIQDIETTESNWRGCRSLQRIHCRS 334
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 DB 395 SDSTVRVNDVNTGEVINTLIHNEAVLHRSNGLMVTCSKDRSTAVNDMASPTDITLRR 454
 QY 358 VLVGHRAAVNVDFDKIVSASGRTTKWSTSTCEVFRTLNHGKRGIAQLQYDRILVV 417
 DB 455 VLVGHRAAVNVDFDKIVSASGRTTKWNTSTCEVFRTLNHGKRGIAQLQYDRILVV 514
 QY 418 SGSSDNTIRLWDIEGACLRVLGHEELVRCIRFQNKIRVSGAYDGKIKVMDLQALDPR 477
 DB 515 SGSSDNTIRLWDIEGACLRVLGHEELVRCIRFQNKIRVSGAYDGKIKVMDLMAALDPR 574

QY 478 APASTLCRLTILVHSGRVFRILQDFQFISSSHDDTILWDFLNVPVPSAQNETRSPSRITY 537
 DB 575 APAGTLCRLTILVHSGRVFRILQDFQFISSSHDDTILWDFLNVPVPSAQNETRSPSRITY 634
 QY 538 TYISR 542
 DB 635 TYISR 639
 RESULT 15
 Q68DSO HUMAN PRELIMINARY; PRT; 564 AA.
 AC Q68DSO;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Hypothetical protein DKFZp781N011.
 GN Name=DKFZp781N011;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RC TISSUE=Amygdala;
 RG The German cDNA Consortium;
 RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; CR749295; CAH18150.1; -; mRNA.
 DR Ensembl; ENSG00000166167; Homo sapiens.
 DR GO; GO:0006512; P:ubiquitin cycle; IEA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; Ubiquitination pathway; WD repeat.
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 Query Match 84.5%; Score 2434; DB 2; Length 564;
 Best Local Similarity 80.5%; Pred. No. 9.1e-172;
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 DB 121 HYQHGHSYLYKPLQDRFITALPARGLDHTAENILSYLDARSLCAAELVCKEWRVTS 180
 QY 161 GMLWKKLIERMVTDPLWKLSERRGWQYLFQKRPDGTG--PPNSFYRSYLPKIIQDIET 218
 DB 181 GMLWKKLIERMVTDPLWKLSERRGWQYLFQKRPDGTG--PPNSFYRSYLPKIIQDIET 240

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Qy	339	DRSIAVMDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEVFT	398
Db	361	DRSIAVMDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEVFT	420
Qy	399	LNGHKRGIACLQYDRDLVSGSSDNTIRLWDIECGACLRVLEEGHEELVRCIRFDNKRIVS	458
Db	421	LNGHKRGIACLQYDRDLVSGSSDNTIRLWDIECGACLRVLEEGHEELVRCIRFDNKRIVS	480
Qy	459	GAYDGKIKVMDLOALDPRAPASTLCRLTLVEHSGRVFRLOFDEFQIISSSHDDTILIMD	518
Db	481	GAYDGKIKVMDLVNALDPRAPAGTLCRLTLVEHSGRVFRLOFDEFQIISSSHDDTILIMD	540
Qy	519	FLNVPPSAQNETRSPSRITYIISR	542
Db	541	FLNDPAAQAEPSPSRITYIISR	564

Search completed: August 25, 2006, 07:22:29
Job time : 307 secs

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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:22:47 ; Search time 50 Seconds
(without alignments)
948.832 Million cell updates/sec

Title: US-10-665-715-16

Perfect score: 2879

Sequence: 1 MEPDSVIEDKTIELMCSVPR.....PPSAQNRTSPRSTYISR 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2879	100.0	542	2	US-09-832-161-16
2	2384.5	82.8	569	2	US-09-832-161-18
3	2384.5	82.8	569	2	US-09-385-219A-2
4	2384.5	82.8	569	2	US-09-601-168B-2
5	2286.5	79.4	517	1	US-08-190-802A-30
6	2286.5	79.4	517	2	US-08-477-346-30
7	2286.5	79.4	517	2	US-08-473-089-30
8	2286.5	79.4	517	2	US-08-487-072A-30
9	643	22.3	626	2	US-09-213-888-21
10	643	22.3	626	2	US-09-328-877D-21
11	641.5	22.3	540	2	US-09-213-888-7
12	641.5	22.3	540	2	US-09-213-888-10
13	641.5	22.3	540	2	US-09-328-877D-7
14	641.5	22.3	540	2	US-09-328-877D-10
15	641.5	22.3	545	2	US-09-213-888-6
16	641.5	22.3	545	2	US-09-328-877D-6
17	641.5	22.3	553	2	US-09-213-888-5
18	641.5	22.3	553	2	US-09-328-877D-5
19	641.5	22.3	559	2	US-09-213-888-9
20	641.5	22.3	559	2	US-09-328-877D-9
21	641.5	22.3	589	2	US-09-213-888-8
22	641.5	22.3	589	2	US-09-328-877D-8
23	641.5	22.3	592	2	US-09-213-888-4
24	641.5	22.3	592	2	US-09-328-877D-4
25	641.5	22.3	627	2	US-09-213-888-3
26	641.5	22.3	627	2	US-09-328-877D-3

ALIGNMENTS

RESULT 1

US-09-832-161-16
; Sequence 16, Application US/09832161
; Patent No. 6656713

GENERAL INFORMATION:

; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Vinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-161-16

Query Match 100.0%; Score 2879; DB 2; Length 542;

Best Local Similarity 100.0%; Pred. No. 6.6e-276;

Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPDSVIEDKTIELMCSVPRSLMGCANLVESMCALSCLOSMPSVRCLOISNGTSSVVS 60

DB 1 MEPDSVIEDKTIELMCSVPRSLMGCANLVESMCALSCLOSMPSVRCLOISNGTSSVVS 60

QY 61 RKRPSGNYQKEDLCIKYFDQMSQDQVFEVHLISRMCHYQHGHSYKPKMLQDFI 120

DB 61 RKRPSGNYQKEDLCIKYFDQMSQDQVFEVHLISRMCHYQHGHSYKPKMLQDFI 120

QY 121 TALPEQGLDHAENILSYLDARSLCAELVCKQWQVISEGMLWKKLIERMVTRDPLWKG 180

DB 121 TALPEQGLDHAENILSYLDARSLCAELVCKQWQVISEGMLWKKLIERMVTRDPLWKG 180

QY 181 LSERRGWDQVLFKNRPTDGPNSFYRLYKPKIOTIETIENNRCCGHNLOQCRSENS 240

DB 181 LSERRGWDQVLFKNRPTDGPNSFYRLYKPKIOTIETIENNRCCGHNLOQCRSENS 240

QY 241 KGVVCLQYDDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGVSCLQYDERVITGSSDS 300

DB 241 KGVVCLQYDDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGVSCLQYDERVITGSSDS 300

QY 27, Appl

DB 27, Appl

QY 25, Appl

DB 25, Appl

QY 314, Appl

DB 314, Appl

QY 14173, A

DB 14173, A

QY 32, Appl

DB 32, Appl

QY 29, Appl

DB 29, Appl

QY 264, App

DB 264, App

QY 8, Appli

DB 8, Appli

QY 18953, A

DB 18953, A

QY 3, Appli

DB 3, Appli

QY 1119, Ap

DB 1119, Ap

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Qy	361	GHRAAVNVVDFDDKVIYVSASGDRTIKWSTSTCFEVRTLNGHKRGIACLQYRDRDLVWSGS	420
Db	361	GHRAAVNVVDFDDKVIYVSASGDRTIKWSTSTCFEVRTLNGHKRGIACLQYRDRDLVWSGS	420
Qy	421	SDNTIRLWDIECGACLRVLBEGHEELVRCIRFDNKRIVSGAVDGKIKVWDLQALDPRAPA	480
Db	421	SDNTIRLWDIECGACLRVLBEGHEELVRCIRFDNKRIVSGAVDGKIKVWDLQALDPRAPA	480
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Db	481	STLCRLTLVEHSGRVFRLOQDFEQIISSSHDDTILIWDFLNVPPSAQNETRSPSRITYYI	540
Qy	541	SR 542	
Db	541	SR 542	

RESULT 2

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US-09-832-161-18
; Sequence 18, Application US/09832161
; Patent No. 6656713
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; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinson
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
;
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF- $\kappa$ B
;
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
;
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;
; LENGTH: 569
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-832-161-18

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Query Match	82.8%;	Score 2384.5;	DB 2;	Length 569;
Best Local Similarity	79.0%;	Pred. No. 6.4e-227;		
Matches 451;	Conservative 48;	Mismatches 41;	Indels 31;	Gaps 7;
Qy	1	MEP--DSVIEDKTIIELMCS-----VP-----RSLWLGCANLV---ESMCAL	36	
Db	1	MDPAEVLQEKALKFMNSREDNCNGEPPRKIIPEKNSLRQTNSCARCLCLNQETVCLA	60	
Qy	37	SCLOSMPSVRLC---QT-SNGTSSVIVSRKPSSENGYQEKDCLCIYKPDQWSESQDVEFE	93	
Db	61	S--TAMKTENCVAKTCLANGTSSMIVPKQKLSASYEKEKELCVKYPQWSESQDVEFE	118	
Qy	94	HLISRMCHYQHGCHINSYLKPMQLQDFITALPEQGLDHIAEINILSYLDARSICAAELVCCKE	153	
Db	119	HLISQMCHYQHGCHINSYLKPMQLQDFITALPARGLDHIAEINILSVLDAKSLCAAELVCCKE	178	
Qy	154	QWRVISEGMLWKKLIERMVRTDPLWGLSERRGWDQYLFKVRPTDG--PPNSSFVRSLYPK	211	
Db	179	WYRVTSDGMLWKKLIERMVRTDLSWRGLAERGMGQYLFKNKPPDPGNAPPNFSYRALYYPK	238	
Qy	212	IIQDIETTESNWRGCRHNLQRCRSENSKGVCYLQYDDERKIIISGLRDNSIKIWDKTSLE	271	

239	IIODIETTESNRCRHSQIHCRESSTKGVCLQYDDQKIVSGURDNITKWDKNITUE	298
272	CLKVLITGHTGVLCLQYDERVIVITGSSDSSTVRVWDVNTGEVLNLTLLHHNEAVLHLRFSNG	331
299	CKRIITGHTGVLCLQYDERVIVITGSSDSSTVRVWDVNTGEMLNTLIHHCEAVLHLRPNNG	358
332	LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVDPDDKYIVSASGDRTIKWMTS	391
359	MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVDPDDKYIVSASGDRTIKWNTS	418
392	TCEFVRTLNHGKRGITACLOYRDLRVSGSSDNITRLWDIECGACLRVLGHEELVRCIRF	451
419	TCEFVRTLNHGKRGITACLOYRDLRVSGSSDNITRLWDIECGACLRVLGHEELVRCIRF	478
452	DNKRIVSGAYDGIKWMDLQALDPRAPASTCLIRTLVEHSGRVFRLQDFEFOIISSSH	511
479	DNKRIVSGAYDGIKWMDLVAALDPRAPAGTCLIRTLVEHSGRVFRLQDFEFOIVSSHD	538
512	DTILTWDFLNVPPSAQNETRSPSRITYIISR	542
539	DTILTWDFLNDPAAQAEPPRSPSRITYIISR	569

RESULT 3

```

US-09-385-219A-2
; Sequence 2, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385.219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-385-219A-2

```

Query Match	82.8%	Score 2384.5	DB 2	Length 569
Best Local Similarity	79.0%	Pred. No. 6.4e-227		
Matches	451	Conservative	48	Mismatches 41
				Indels 31
				Gaps 7

QY 272 CLKVLTGHTGSLVCLQYDERVIVTSSDSTVRVWVNDVTGEVNTLIHHNEAVLHLRFSNG 331
DB 299 CKRILTGTGSLVCLQYDERVIVTSSDSTVRVWVNDVTGEVNTLIHHNEAVLHLRFSNG 358
QY 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRRTIKVWSTS 391
DB 359 MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRRTIKVWSTS 418
QY 392 TCEVFTLNGHKGRIACIQLYDRDLVVGSSDNTIRLWDIECGACLRVLEGEHEELVRCIRF 451
DB 419 TCEVFTLNGHKGRIACIQLYDRDLVVGSSDNTIRLWDIECGACLRVLEGEHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKIKVWDLQALDPRAPASTLCRLTLVEHSGRVPRLOFDFQIISSHD 511
DB 479 DNKRIVSGAYDGKIKVWDLVAAALDPRAPAGTLCRLTLVEHSGRVPRLOFDFQIISSHD 538
QY 512 DTILWDFLNVPPSAQNTRSPSRTTYISR 542
DB 539 DTILWDFLNDPAAQAEPSPSRTTYISR 569
RESULT 4
US-09-601-168B-2
; Sequence 2, Application US/09601168B
; Patent No. 6730486
; GENERAL INFORMATION:
; APPLICANT: BENAROUS, Richard
; APPLICANT: MARGOTTIN, Florence
; APPLICANT: DURAND, Hervé
; APPLICANT: ARENZANA SEISDEDOS, Fernando
; APPLICANT: KROLL, Mathias
; APPLICANT: CONDORCET, Jean-Paul
; TITLE OF INVENTION: Human beta-TrCP protein
; FILE REFERENCE: 935.38812X00
; CURRENT APPLICATION NUMBER: US/09/601,168B
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: PCT/FR99/00196
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: FR98 01100
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR98 15545
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1 and manually
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence : cDNA
; OTHER INFORMATION: coding for human beta-TrCP protein
US-09-601-168B-2
Query Match 82.8%; Score 2384.5; DB 2; Length 569;
Best Local Similarity 79.0%; Pred. No. 6.4e-227;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
DB 1 MDPAAVLQKALKFNMSSEREDCNGGPPPKKIPEKNSLRQTYNSCARCLNQETVCLA 60
QY 37 SCLQSMPSVRL---QISNGTSSVTSVRKSEGNVQKEKDCIKYFDWSESQVEVE 93
DB 61 S--TAMKTENCVAKTKLANGTSSMTVPKORKLSASYEKEKELCVKYPQWSESQVEVE 118
QY 94 HLISRMCHYQGHINSYKPKMLQDFITALPEQGLDHAENILSYLDARSICAELVCKE 153
DB 119 HLISQCHYQGHINSYKPKMLQDFITALPARGLDHAENILSYLDAKSICAELVCKE 178
QY 154 WORVISGMLWKGLIERMVRTDPLWKGLSERGGWDQYLFKRNPTDG--PPNSFYRSLYPK 211
DB 179 WYRVTSQGLWKGLIERMVRTDSLWRGLAERRGQYLFKKNKPPDGNAPPNSFYRSLYPK 238

QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRDNISIKIWDKITSLE 271
DB 239 IIQDIETIESNRCGRHNLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNITIKIWDKNTLE 298
QY 272 CLKVLTGHTGSLVCLQYDERVIVTSSDSTVRVWVNDVTGEVNTLIHHNEAVLHLRFSNG 331
DB 299 CKRILTGTGSLVCLQYDERVIVTSSDSTVRVWVNDVTGEVNTLIHHCEAVLHLRFSNG 358
QY 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRRTIKVWSTS 391
DB 359 MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRRTIKVWSTS 418
QY 392 TCEVFTLNGHKGRIACIQLYDRDLVVGSSDNTIRLWDIECGACLRVLEGEHEELVRCIRF 451
DB 419 TCEVFTLNGHKGRIACIQLYDRDLVVGSSDNTIRLWDIECGACLRVLEGEHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKIKVWDLQALDPRAPASTLCRLTLVEHSGRVPRLOFDFQIISSHD 511
DB 479 DNKRIVSGAYDGKIKVWDLVAAALDPRAPAGTLCRLTLVEHSGRVPRLOFDFQIISSHD 538
QY 512 DTILWDFLNVPPSAQNTRSPSRTTYISR 542
DB 539 DTILWDFLNDPAAQAEPSPSRTTYISR 569
RESULT 5
US-08-190-802A-30
; Sequence 30, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-190-802A-30
Query Match 79.4%; Score 2286.5; DB 1; Length 517;
Best Local Similarity 87.8%; Pred. No. 2.8e-217;

Matches	423;	Conservative	33;	Mismatches	23;	Indels	3;	Gaps	2;
Qy	44	SVRCLOISNGTSSVIVSRKRPSEGNVQKEKDLCKIFYDQMSQSEQVFEVHLSRMCHYQ	103	:	:	:	:	:	:
Db	34	TLRQTKLANGTSSMIVPKQKLSANYEKEKELCVKYFEQMSQSEQVFEVHLSRMCHYQ	93	:	:	:	:	:	:
Qy	104	HGHTSYLKPMLQRDFITALPEQGLDHIHAENILSYLDAARSLCAELVCKEQRVISEGML	163	:	:	:	:	:	:
Db	94	HGHTSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAELVCKEQRVYTSQML	153	:	:	:	:	:	:
Qy	164	WKKLIERMVRTDPLWGLSERRGHWQVLFKNRPTDG--PNSFVRSLYPKLIQDIETIES	221	:	:	:	:	:	:
Db	154	WKKLIERMVRTDLSWRGLAERGWQVLFKNKPPDGKTPPNSFYRALYPKLIQDIETIES	213	:	:	:	:	:	:
Qy	222	NWRCGRINLQRIQCRSENSKVYCLQYDDDEKIIISGLRDNISIKIWDKTSLECLKVLTGHTG	281	:	:	:	:	:	:
Db	214	NWRCGRHSLQRIHCRSETSKVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTG	273	:	:	:	:	:	:
Qy	282	SVLCLOYDERVIVTSGSSDSTVVRVMDVNTGEVNTLIHHNEAVLHLRFSNGLMWVTCSDKRS	341	:	:	:	:	:	:
Db	274	SVLCLOYDERVIVTSG--SDSTVVRVMDVNTGEMLNTLIHHCEAVLHLRFSNGLMWVTCSDKRS	332	:	:	:	:	:	:
Qy	342	IAVWDMASATDITLRRVLVGHRAAVNVVDPDKIVVSAGDRTIKVWSTSTCEFVRTLNG	401	:	:	:	:	:	:
Db	333	IAVWDMASATDITLRRVLVGHRAAVNVVDFDKIVVSAGDRTIKVWNTSTCEFVRTLNG	392	:	:	:	:	:	:
Qy	402	HKRGICLOYRDRILVWSSSDNTIRLWDIECGACLRVLLEGHEELVRCIRFONKRIVSGAY	461	:	:	:	:	:	:
Db	393	HKRGICLOYRDRILVWSSSDNTIRLWDIECGACLRVLLEGHEELVRCIRFONKRIVSGAY	452	:	:	:	:	:	:
Qy	462	DGKIKVMDLQAALDPAPASTLCRLTLVEHSGRVRFLQDFEQIISSSHDDTILIWDFLN	521	:	:	:	:	:	:
Db	453	DGKIKVMDLVNALLDPAPAGTLCRLTLVEHSGRVRFLQDFEQIVSSSHDDTILIWDFLN	512	:	:	:	:	:	:
Qy	522	VP 523							
Db	513	DP 514							

RESULT 6
US-08-477-346-30
Sequence 30, Application US/09477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WP-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match 79.4%; Score 2286.5; DB 2; Length 517;
Best Local Similarity 87.8%; Pred. No. 2.8e-217;
Matches 423; Conservative 33; Mismatches 23; Indels 3; Caps 2;
QY 44 SVRCLOISNGTSVIVSRKPSGEGYQKDLCKIKYFDQWSESDQVEFVEHLISRMCHQ 103
DB 34 TLKQTKLANGTSMIVPKORLSANYEKEKELCVKFEQMSQCDQVEFVEHLISRMCHQ 93
QY 104 HGHINSYLPMLQORDFITALPEQGLDHAENILSYLDARSCLAAELVCKEWRVISEGML 163
DB 94 HGHINTYLPMLQORDFITALPARGLDHAENILSYLDARSCLAAELVCKEWRVISEGML 153
QY 164 WKKLIERMVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRLYPKIIODIETIES 221
DB 154 WKKLIERMVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRLYPKIIODIETIES 213
QY 222 NRCGRHNLQROCRSENSGVYQYDDEKIIISGLRDNISIKIWDKTSLECLVLTGHTG 281
DB 214 NRCGRHNLQROCRSENSGVYQYDDEKIIISGLRDNISIKIWDKTSLECLVLTGHTG 273
QY 282 SVLCLOYDERVITGSDSTVRVMDVNTGEVLTNLIHNEAVLHRLFSNGLMVTCSKDRS 341
DB 274 SVLCLOYDERVITGSDSTVRVMDVNTGEVLTNLIHNEAVLHRLFSNGLMVTCSKDRS 332
QY 342 IAWDMASATDITLRRVLVGHRAAVNVVDFDDKIIIVSASGDRTIKVMSTSTCEFVRLNG 401
DB 333 IAWDMASATDITLRRVLVGHRAAVNVVDFDDKIIIVSASGDRTIKVMSTSTCEFVRLNG 392
QY 402 HKRGIAQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHBEELVRCIFDNKRIYSGAY 461
DB 393 HKRGIAQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHBEELVRCIFDNKRIYSGAY 452
QY 462 DGKIKVWDIQAALDPRAPASTLCRLTLVHSGRVFRLQFDFEQIIVSSSHDDTILIWDFFLN 521
DB 522 VP 523
DB 513 DP 514

RESULT 8
US-08-487-072A-30
; Sequence 30, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match 79.4%; Score 2286.5; DB 2; Length 517;
Best Local Similarity 87.8%; Pred. No. 2.8e-217;
Matches 423; Conservative 33; Mismatches 23; Indels 3; Caps 2;
QY 44 SVRCLOISNGTSVIVSRKPSGEGYQKDLCKIKYFDQWSESDQVEFVEHLISRMCHQ 103
DB 34 TLKQTKLANGTSMIVPKORLSANYEKEKELCVKFEQMSQCDQVEFVEHLISRMCHQ 93
QY 104 HGHINSYLPMLQORDFITALPEQGLDHAENILSYLDARSCLAAELVCKEWRVISEGML 163
DB 94 HGHINTYLPMLQORDFITALPARGLDHAENILSYLDARSCLAAELVCKEWRVISEGML 153
QY 164 WKKLIERMVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRLYPKIIODIETIES 221
DB 154 WKKLIERMVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRLYPKIIODIETIES 213
QY 222 NRCGRHNLQROCRSENSGVYQYDDEKIIISGLRDNISIKIWDKTSLECLVLTGHTG 281
DB 214 NRCGRHNLQROCRSENSGVYQYDDEKIIISGLRDNISIKIWDKTSLECLVLTGHTG 273
QY 282 SVLCLOYDERVITGSDSTVRVMDVNTGEVLTNLIHNEAVLHRLFSNGLMVTCSKDRS 341
DB 274 SVLCLOYDERVITGSDSTVRVMDVNTGEVLTNLIHNEAVLHRLFSNGLMVTCSKDRS 332
QY 342 IAWDMASATDITLRRVLVGHRAAVNVVDFDDKIIIVSASGDRTIKVMSTSTCEFVRLNG 401
DB 333 IAWDMASATDITLRRVLVGHRAAVNVVDFDDKIIIVSASGDRTIKVMSTSTCEFVRLNG 392
QY 402 HKRGIAQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHBEELVRCIFDNKRIYSGAY 461
DB 393 HKRGIAQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHBEELVRCIFDNKRIYSGAY 452
QY 462 DGKIKVWDIQAALDPRAPASTLCRLTLVHSGRVFRLQFDFEQIIVSSSHDDTILIWDFFLN 521

Db 453 DGKIKVLDVAALDPRAPAGTLCRLTLVHSGRFRLODFBQIVSSSHDDTLIWDPLN 512
QY 522 VP 523
Db 513 DP 514

RESULT 9
US-09-213-888-21
; Sequence 21, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
; OTHER INFORMATION: homo sapien
US-09-213-888-21

Query Match 22.3%; Score 643; DB 2; Length 626;
Best Local Similarity 30.2%; Pred. No. 1.9e-54;
Matches 163; Conservative 101; Mismatches 210; Indels 66; Gaps 15;
QY 4 DSVIEDKTI--ELMCSVPRSLWLGA---NLVESMCALS-----CLQSMPSVRC 47
Db 71 DLTMEQKLISEEDLNSMKRKLHGSEVRSFSLGKKPKVSEYTSVTGLVPCSATPTTFGD 130
QY 48 LOISNGTSSVIVSRK-----PSEGNVQKEDLCIKYFDQWSESDQVFEVHLSRMCHY 102
Db 131 LRAANGQGO---QRRRITSVQPTGLQE-----WLKMFQSWGPEKLLALDELIDSCPT 182
QY 103 QGHINSYLPKMLQRFITALPEOGLDHIENILSYLDARSICAAELVCKEWQVISEGM 162
Db 183 QVKKHMQVIEPQFQDFISLLPKE-----LALYVLSFLEPKDLQAAQTCRYW-RILAEDN 237
QY 163 LWKKLIERMVRTDPLWKGLSERRGWDQYL-FKNRPTDGPNSFYRSLYPKIIQDIETIES 221
Db 238 L-----LWRECKEKGIDEPHLHKKRKVIKP--GFHSPKMSAYIRQHRIDT 282
QY 222 NWRGGRHNLQRCRSENSKGVYCLQYDDEKIIISGLRDNISIKWDTSLKLVLTGHTG 281
Db 283 NWRGELKSPKV-LKGHDHVTICLQFCGNRIVSGSDNTLKWSAVTKCLRTLVGHTG 341
QY 282 SVLCQYDERVIVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHRLFNSGLMVTCSKORS 341
Db 342 GWSSQMRNIIISGSTDRTLKVNNAETGECIHTLYGHTSTVRCMHLEKRVVSGSRDAT 401
QY 342 IAWDMASATDITLRLVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEFTVTLNG 401
Db 402 LRWVDIETGQCL---HVLMGHVAARVQVQDGRVVSAGYDFWVKWDPETETCLHTLQ 458
QY 402 HKRGACIQLYRDLRVVSGSDNTIRLWDIECGACLRVLEGHBEELVRCIRFDNKRIVSGAY 461
Db 459 HTNRVVSLOFDGIHVVSGLDTSIRVWDVETGNCIHTLTGHOSLTSGMELKONILVSGNA 518
QY 462 DGKIKVLDQAALDPRAPASTLCRLTLV---EHSGRVFRLODFBQIVSSSHDDTLIWD 518
Db 519 DSTVKIWDIKTG-----QCLQTLQGNKHSQAVTCLQFNKNFVITSSDDGTGKVLWD 569

RESULT 10
US-09-328-877D-21
; Sequence 21, Application US/09328877D
; Patent No. 6730778
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877D
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
; OTHER INFORMATION: homo sapien
US-09-328-877D-21

Query Match 22.3%; Score 643; DB 2; Length 626;
Best Local Similarity 30.2%; Pred. No. 1.9e-54;
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QY 4 DSVIEDKTI--ELMCSVPRSLWLGA---NLVESMCALS-----CLQSMPSVRC 47
Db 71 DLTMEQKLISEEDLNSMKRKLHGSEVRSFSLGKKPKVSEYTSVTGLVPCSATPTTFGD 130
QY 48 LOISNGTSSVIVSRK-----PSEGNVQKEDLCIKYFDQWSESDQVFEVHLSRMCHY 102
Db 131 LRAANGQGO---QRRRITSVQPTGLQE-----WLKMFQSWGPEKLLALDELIDSCPT 182
QY 103 QGHINSYLPKMLQRFITALPEOGLDHIENILSYLDARSICAAELVCKEWQVISEGM 162
Db 183 QVKKHMQVIEPQFQDFISLLPKE-----LALYVLSFLEPKDLQAAQTCRYW-RILAEDN 237
QY 163 LWKKLIERMVRTDPLWKGLSERRGWDQYL-FKNRPTDGPNSFYRSLYPKIIQDIETIES 221
Db 238 L-----LWRECKEKGIDEPHLHKKRKVIKP--GFHSPKMSAYIRQHRIDT 282
QY 222 NWRGGRHNLQRCRSENSKGVYCLQYDDEKIIISGLRDNISIKWDTSLKLVLTGHTG 281
Db 283 NWRGELKSPKV-LKGHDHVTICLQFCGNRIVSGSDNTLKWSAVTKCLRTLVGHTG 341
QY 282 SVLCQYDERVIVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHRLFNSGLMVTCSKORS 341
Db 342 GWSSQMRNIIISGSTDRTLKVNNAETGECIHTLYGHTSTVRCMHLEKRVVSGSRDAT 401
QY 342 IAWDMASATDITLRLVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEFTVTLNG 401
Db 402 LRWVDIETGQCL---HVLMGHVAARVQVQDGRVVSAGYDFWVKWDPETETCLHTLQ 458
QY 402 HKRGACIQLYRDLRVVSGSDNTIRLWDIECGACLRVLEGHBEELVRCIRFDNKRIVSGAY 461
Db 459 HTNRVVSLOFDGIHVVSGLDTSIRVWDVETGNCIHTLTGHOSLTSGMELKONILVSGNA 518
QY 462 DGKIKVLDQAALDPRAPASTLCRLTLV---EHSGRVFRLODFBQIVSSSHDDTLIWD 518
Db 519 DSTVKIWDIKTG-----QCLQTLQGNKHSQAVTCLQFNKNFVITSSDDGTGKVLWD 569

RESULT 11
US-09-213-888-7
; Sequence 7, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.


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Qy 196 PTGPPNSFYRSLYPKIIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIS 255
Db 173 KVIKP--GFIHSPWKSAYIROHRIDTNWRRGELKSPKV-LKGHDDHVTICLQFCGNRIVS 229
Qy 256 GLRNSIKIWDKTSLECLKVLGTGHTGSLVLCIQLYDERVIVTGSSTVVRVMDVNTGEVLNT 315
Db 230 GSDNTLKWSAVTGKCLRTLVGHTGGVSSQMRDNIISGSTDRTLKVNNAETGECIHT 289
Qy 316 LIHNEAVLHLRFSNGLMVTCKDRSIAVMDMASATDITLRRVLVGHRAAVNVVDFDDKY 375
Db 290 LYGTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL--HVLMGHVAARVCVQYDGR 346
Qy 376 IVSASGDRTIKWSTSTCFVRLNGHKGRIACLOYDRRLVVGSSDNTIRLWDIECGAC 435
Db 347 VVSGAYDFMWKVPDPTETCLHTLQGHTRNVYSLQFDGIHVVGSLDTSIRVMDVETGNC 406
Qy 436 LRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTV---BHS 492
Db 407 IHTLTGHOSLTSGMELKNILVSGNADSTVKIWDIKTG-----OCLQTLQGPKNKHQ 457
Qy 493 GRVFRLOQDFEQIISSSHDDTILIWD 518
Db 458 SAVTCLQFNKNFVITSSDDGTIVKLWD 483
Qy 436 LRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTV---BHS 492
Db 407 IHTLTGHOSLTSGMELKNILVSGNADSTVKIWDIKTG-----OCLQTLQGPKNKHQ 457
Qy 493 GRVFRLOQDFEQIISSSHDDTILIWD 518
Db 458 SAVTCLQFNKNFVITSSDDGTIVKLWD 483
RESULT 14
US-09-328-877D-10
; Sequence 10, Application US/09328877D
; Patent No. 6730778
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877D
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877D-10
Query Match 22.3%; Score 641.5; DB 2; Length 540;
Best Local Similarity 32.1%; Pred. No. 2.1e-54;
Matches 143; Conservative 89; Mismatches 177; Indels 37; Gaps 9;
Qy 77 IKYFDQWSESDQVEFVEHLISRMCHYQGHINSYLPKMLQDRDIFITALPEQGLDHAENIL 136
Db 71 LKMFQSWSGPEKLLALDELIDSCPTQVKHMVQIEPQFQRFISLLPKE----LALYVL 126
Qy 137 SYLDARSLCAALVCKEQRVISEGMLWKLIERMVTRDPLWKLGSERRGWDQYL-FKOR 195
Db 127 SFLEPKDLQAQTCRYW-RILAEDNL-----LWRECKKEGIDEPLHIKR 172
Qy 196 PTGPPNSFYRSLYPKIIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIS 255
Db 173 KVIKP--GFIHSPWKSAYIROHRIDTNWRRGELKSPKV-LKGHDDHVTICLQFCGNRIVS 229
Qy 256 GLRNSIKIWDKTSLECLKVLGTGHTGSLVLCIQLYDERVIVTGSSTVVRVMDVNTGEVLNT 315
Db 230 GSDNTLKWSAVTGKCLRTLVGHTGGVSSQMRDNIISGSTDRTLKVNNAETGECIHT 289
Qy 316 LIHNEAVLHLRFSNGLMVTCKDRSIAVMDMASATDITLRRVLVGHRAAVNVVDFDDKY 375
Db 290 LYGTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL--HVLMGHVAARVCVQYDGR 346
Qy 376 IVSASGDRTIKWSTSTCFVRLNGHKGRIACLOYDRRLVVGSSDNTIRLWDIECGAC 435
Db 347 VVSGAYDFMWKVPDPTETCLHTLQGHTRNVYSLQFDGIHVVGSLDTSIRVMDVETGNC 406
Qy 436 LRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTV---BHS 492
Db 407 IHTLTGHOSLTSGMELKNILVSGNADSTVKIWDIKTG-----OCLQTLQGPKNKHQ 457
Qy 493 GRVFRLOQDFEQIISSSHDDTILIWD 518
Db 458 SAVTCLQFNKNFVITSSDDGTIVKLWD 483
RESULT 15
US-09-213-888-6
; Sequence 6, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-6
Query Match 22.3%; Score 641.5; DB 2; Length 545;
Best Local Similarity 32.1%; Pred. No. 2.1e-54;
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Qy 77 IKYFDQWSESDQVEFVEHLISRMCHYQGHINSYLPKMLQDRDIFITALPEQGLDHAENIL 136
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Qy 137 SYLDARSLCAALVCKEQRVISEGMLWKLIERMVTRDPLWKLGSERRGWDQYL-FKOR 195
Db 132 SFLEPKDLQAQTCRYW-RILAEDNL-----LWRECKKEGIDEPLHIKR 177
Qy 196 PTGPPNSFYRSLYPKIIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIS 255
Db 178 KVIKP--GFIHSPWKSAYIROHRIDTNWRRGELKSPKV-LKGHDDHVTICLQFCGNRIVS 234
Qy 256 GLRNSIKIWDKTSLECLKVLGTGHTGSLVLCIQLYDERVIVTGSSTVVRVMDVNTGEVLNT 315
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Qy 316 LIHNEAVLHLRFSNGLMVTCKDRSIAVMDMASATDITLRRVLVGHRAAVNVVDFDDKY 375
Db 295 LYGTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL--HVLMGHVAARVCVQYDGR 351
Qy 376 IVSASGDRTIKWSTSTCFVRLNGHKGRIACLOYDRRLVVGSSDNTIRLWDIECGAC 435
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Qy 436 LRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTV---BHS 492
Db 412 IHTLTGHOSLTSGMELKNILVSGNADSTVKIWDIKTG-----OCLQTLQGPKNKHQ 462
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RESULT 15
US-09-213-888-6
; Sequence 6, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-6
Query Match 22.3%; Score 641.5; DB 2; Length 545;
Best Local Similarity 32.1%; Pred. No. 2.1e-54;
Matches 143; Conservative 89; Mismatches 177; Indels 37; Gaps 9;
Qy 77 IKYFDQWSESDQVEFVEHLISRMCHYQGHINSYLPKMLQDRDIFITALPEQGLDHAENIL 136
Db 76 LKMFQSWSGPEKLLALDELIDSCPTQVKHMVQIEPQFQRFISLLPKE----LALYVL 131
Qy 137 SYLDARSLCAALVCKEQRVISEGMLWKLIERMVTRDPLWKLGSERRGWDQYL-FKOR 195
Db 132 SFLEPKDLQAQTCRYW-RILAEDNL-----LWRECKKEGIDEPLHIKR 177
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Qy 376 IVSASGDRTIKWSTSTCFVRLNGHKGRIACLOYDRRLVVGSSDNTIRLWDIECGAC 435
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Job time : 51 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:34:43 ; Search time 185 Seconds
(without alignments)
1357.094 Million cell updates/sec

Title: US-10-665-715-16
Perfect score: 2879
Sequence: 1 MEPDSVIEDKTIELMCSVPR.....PPSAQNTRSPSRITYISR 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC Celler SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC Celler SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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6: /EMC Celler SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2879	100.0	542	3	US-09-832-161-16 Sequence 16, Appl
2	2879	100.0	542	4	US-10-665-715-16 Sequence 16, Appl
3	2384.5	82.8	569	3	US-09-832-161-18 Sequence 18, Appl
4	2384.5	82.8	569	4	US-10-665-715-18 Sequence 18, Appl
5	2384.5	82.8	569	4	US-10-042-417-2 Sequence 2, Appl
6	2384.5	82.8	569	4	US-10-038-010-8 Sequence 8, Appl
7	2384.5	82.8	569	4	US-10-665-715-18 Sequence 18, Appl
8	2384.5	82.8	569	5	US-10-652-928-2 Sequence 2, Appl
9	2384.5	82.8	569	5	US-10-632-150-2 Sequence 2, Appl
10	2384.5	82.8	569	6	US-11-073-470-2 Sequence 2, Appl
11	2384.5	82.8	569	6	US-11-073-457-2 Sequence 2, Appl
12	2384.5	82.8	569	6	US-11-099-691-12 Sequence 12, Appl
13	2384.5	82.8	569	6	US-11-073-460-2 Sequence 2, Appl
14	2375.5	82.5	569	4	US-10-687-732-18 Sequence 18, Appl
15	2077.5	72.2	510	6	US-11-097-143-6363 Sequence 6363, Ap
16	2002	69.5	408	4	US-10-687-732-15 Sequence 15, Appl
17	1829.5	63.5	407	4	US-10-687-732-14 Sequence 14, Appl
18	1638.5	56.9	701	4	US-10-369-493-5420 Sequence 5420, Ap
19	1525	53.0	424	4	US-10-687-732-13 Sequence 13, Appl
20	1143	39.7	265	3	US-09-764-848-30 Sequence 30, Appl
21	1143	39.7	265	4	US-10-116-016-30 Sequence 30, Appl
22	1143	39.7	265	4	US-10-222-020-30 Sequence 30, Appl
23	693.5	24.1	239	4	US-10-023-530-2 Sequence 2, Appl
24	654	22.7	1326	6	US-11-097-143-28503 Sequence 28503, A
25	654	22.7	1326	6	US-11-097-143-28506 Sequence 28506, A
26	654	22.7	1326	6	US-11-097-143-36945 Sequence 36945, A
27	643	22.3	626	3	US-09-213-888-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1

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US-09-832-161-16
; Sequence 16, Application US/09832161
; Publication No. US20030166587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-16

Query Match      100.0%; Score 2879; DB 3; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.3e-244;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61  RRPESGNYQKEXDLCIKYFDQWSESDQVEFVEHLISRMCHYQGHINSYLKPMQLQDFI 120
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Qy      121  TALPEQGLDHIAENILSYLDARSALCAELVCKEQRVISEGMLWKKLIERMVTDPLWKG 180
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Db      121  TALPEQGLDHIAENILSYLDARSALCAELVCKEQRVISEGMLWKKLIERMVTDPLWKG 180
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Qy      181  LSERRGWDQVLFKNRPTDGPNNFYRSLPKIIDIETTESNWRGHRHLQRCSENS 240
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Db      181  LSERRGWDQVLFKNRPTDGPNNFYRSLPKIIDIETTESNWRGHRHLQRCSENS 240
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 Qy 452 DNKRIVSGAYDGGIKI KWDLOAALDPRAPASTLCRLTVEHSGRVFRQLQDFEFOIISSSH 511
 Db 479 DNKRIVSGAYDGGIKI KWDLVAAALDPRAPAGTLCRLTVEHSGRVFRQLQDFEFOIISSSH 538
 Qy 512 DTILIWDFLNVPPSAQNETRSPSRITYISR 542
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RESULT 4
 US-10-042-417-2
 ; Sequence 2, Application US/10042417
 ; Publication No. US20020123082A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, M.
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
 ; FILE REFERENCE: 5914-090-999
 ; CURRENT APPLICATION NUMBER: US/10/042,417
 ; CURRENT FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 60/260,179
 ; PRIOR FILING DATE: 2001-01-5
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-042-417-2

Query Match 82.8%; Score 2384.5; DB 4; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 Qy 1 MEP-DSVIDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 Db 1 MDPAEAVLQKALKFNNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARCLNQETVCLA 60
 Qy 37 SCLQSMPSVRCL---QISNGTSSVIVSRKPSBGNYOKEKDLCKIKYFDOWSESQDVEFVE 93
 Db 61 S--TAMKTENCVAKTLANGTSSMIVPKQKLSASVEKEKELCVKVFQWSESQDVEFVE 118
 Qy 94 HLISRMCHYQHGHINSYLPMLQDFITALPEOGLDHIHAEINILSYLDARSLCAELVCKE 153
 Db 119 HLISOMCHYQHGHINSYLPMLQDFITALPARGLDHIHAEINILSYLDAKSLCAELVCKE 178
 Qy 154 WQVISEGLMWKLLIERMVRTDPLWGLSERRGWDQYLFKNRPTDG--PNSFYRSIYLPK 211
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 Qy 512 DTILIWDFLNVPPSAQNETRSPSRITYISR 542
 Db 539 DTILIWDFLNDPAQAEPSPSRITYISR 569

RESULT 5
 US-10-038-010-8
 ; Sequence 8, Application US/10038010
 ; Publication No. US20030040089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYBRIGENICS
 ; APPLICANT: Pierre, Legrain
 ; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
 ; FILE REFERENCE: B4767A
 ; CURRENT APPLICATION NUMBER: US/10/038,010
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 60/259,377
 ; PRIOR FILING DATE: 2001-01-02
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: beta-TrCP1
 ; LOCATION: (1)..(569)
 ; OTHER INFORMATION:
 US-10-038-010-8

Query Match 82.8%; Score 2384.5; DB 4; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 Qy 1 MEP-DSVIDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 Db 1 MDPAEAVLQKALKFNNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARCLNQETVCLA 60
 Qy 37 SCLQSMPSVRCL---QISNGTSSVIVSRKPSBGNYOKEKDLCKIKYFDOWSESQDVEFVE 93
 Db 61 S--TAMKTENCVAKTLANGTSSMIVPKQKLSASVEKEKELCVKVFQWSESQDVEFVE 118
 Qy 94 HLISRMCHYQHGHINSYLPMLQDFITALPEOGLDHIHAEINILSYLDARSLCAELVCKE 153
 Db 119 HLISOMCHYQHGHINSYLPMLQDFITALPARGLDHIHAEINILSYLDAKSLCAELVCKE 178
 Qy 154 WQVISEGLMWKLLIERMVRTDPLWGLSERRGWDQYLFKNRPTDG--PNSFYRSIYLPK 211
 Db 179 WYRVTSDGLMWKLLIERMVRTDPLWGLSERRGWDQYLFKNRPTDG--PNSFYRSIYLPK 238
 Qy 212 IIQDIETIESNRCGRHSLQRIHCRSETSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 271
 Db 239 IIQDIETIESNRCGRHSLQRIHCRSETSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 298
 Qy 272 CLAVLGTGTSVLCQYDERVIVTGSSDSTVRVMDVNTGEVLTNLIHNEAVLHLRFSNG 331
 Db 299 CKRILGTGTSVLCQYDERVIVTGSSDSTVRVMDVNTGEVLTNLIHNEAVLHLRFSNG 358
 Qy 332 LMVTCSDRSIAVMDNASATDITLRLVVGHRAAVNVVDFDDKYIVSASGDRTIKWSTS 391
 Db 359 MMVTCSDRSIAVMDNASPTDITLRLVVGHRAAVNVVDFDDKYIVSASGDRTIKWSTS 418

QY 392 TCEFVRTLNHGKRGIAQLQYRDLRVVSGSSDNTIRLWDIECGACLRVLGEGHEELVRCIRF 451
DB 419 TCEFVRTLNHGKRGIAQLQYRDLRVVSGSSDNTIRLWDIECGACLRVLGEGHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCRLTLVEHSGRVFRLQDFQFISSHD 511
DB 479 DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCRLTLVEHSGRVFRLQDFQFISSHD 538
QY 512 DTILWDFLNVPPSAQNETRSPSRTTYISR 542
DB 539 DTILWDFLNDPAQAEPSPSRTTYISR 569
RESULT 6
US-10-665-715-18
; Sequence 18, Application US/10665715
; Publication No. US20040203098A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Irit
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF-kB
; CURRENT FILING DATE: 2003-09-19
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/10/665,715
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-665-715-18

Query Match 82.8%; Score 2384.5; DB 4; Length 569;
Best Local Similarity 79.0%; Pred. No. 5.3e-201;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
DB 1 MDPAEAVLQEKALKFPMNSEREDCNNGEPKRIIPEKNSLRQTYNSCARCLNQETVCLA 60
QY 37 SCLQSMPSVRCJL---QISNGTSSVIVSRKRPSEGVYQKEKOLCIKYFDQWSESDDQVEFVE 93
DB 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYFQWSESDDQVEFVE 118
QY 94 HLISRMCHYQGHINSYLPKMLQDFITALPQGLDHAENILSYLDARSICAALVCKE 153
DB 119 HLISQCHYQGHINSYLPKMLQDFITALPARGLDHAENILSYLDARSLCAALVCKE 178
QY 154 WQVIVSEGMLWKKLIERMVVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYSLYPK 211
DB 179 WYRVTSQGLMWWKLIERMVVRTDSLWGLAERGMGQYLFKNKPPDGNAPPNSFYALYPK 238
QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRNSIKIWDKTSLE 271
DB 239 IIQDIETIESNRCGRHSLQRIHCRSETSKGVYCLQYDQKIVSGLRDNTIKIWDKNTLE 298
QY 272 CLKVLTGHTGSLVCLQYDERVITVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHLRFPNG 331
DB 299 CKRIILTGTGSLVCLQYDERVITVTGSSDSTVRVWDVNTGEMTLTIHCEAVLHLRFPNG 358
QY 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWMTS 391
DB 359 MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWMTS 418

QY 392 TCEFVRTLNHGKRGIAQLQYRDLRVVSGSSDNTIRLWDIECGACLRVLGEGHEELVRCIRF 451
DB 419 TCEFVRTLNHGKRGIAQLQYRDLRVVSGSSDNTIRLWDIECGACLRVLGEGHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCRLTLVEHSGRVFRLQDFQFISSHD 511
DB 479 DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCRLTLVEHSGRVFRLQDFQFISSHD 538
QY 512 DTILWDFLNVPPSAQNETRSPSRTTYISR 542
DB 539 DTILWDFLNDPAQAEPSPSRTTYISR 569
RESULT 7
US-10-652-928-2
; Sequence 2, Application US/10652928
; Publication No. US20050079558A1
; GENERAL INFORMATION:
; APPLICANT: Chiaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/652,928
; CURRENT FILING DATE: 2003-08-28
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-928-2

Query Match 82.8%; Score 2384.5; DB 5; Length 569;
Best Local Similarity 79.0%; Pred. No. 5.3e-201;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
DB 1 MDPAEAVLQEKALKFPMNSEREDCNNGEPKRIIPEKNSLRQTYNSCARCLNQETVCLA 60
QY 37 SCLQSMPSVRCJL---QISNGTSSVIVSRKRPSEGVYQKEKOLCIKYFDQWSESDDQVEFVE 93
DB 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYFQWSESDDQVEFVE 118
QY 94 HLISRMCHYQGHINSYLPKMLQDFITALPQGLDHAENILSYLDARSICAALVCKE 153
DB 119 HLISQCHYQGHINSYLPKMLQDFITALPARGLDHAENILSYLDARSLCAALVCKE 178
QY 154 WQVIVSEGMLWKKLIERMVVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYSLYPK 211
DB 179 WYRVTSQGLMWWKLIERMVVRTDSLWGLAERGMGQYLFKNKPPDGNAPPNSFYALYPK 238
QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRNSIKIWDKTSLE 271
DB 239 IIQDIETIESNRCGRHSLQRIHCRSETSKGVYCLQYDQKIVSGLRDNTIKIWDKNTLE 298
QY 272 CLKVLTGHTGSLVCLQYDERVITVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHLRFPNG 331
DB 299 CKRIILTGTGSLVCLQYDERVITVTGSSDSTVRVWDVNTGEMTLTIHCEAVLHLRFPNG 358
QY 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWMTS 391
DB 359 MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWMTS 418

QY 392 TCEVFTLNGHKGACIACQYRDLRVVSGSSDNTIRLWDIECGACIACLRVLGHEELVRCIRF 451
 DB 419 TCEVFTLNGHKGACIACQYRDLRVVSGSSDNTIRLWDIECGACIACLRVLGHEELVRCIRF 478
 QY 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRITLVHSGRVRFLQDFEQIISSSH 511
 DB 479 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRITLVHSGRVRFLQDFEQIISSSH 538
 QY 512 DTILWDFLNVPPSAQNETRSPSRITYISR 542
 DB 539 DTILWDFLNDPAQAEPSPSRITYISR 569

RESULT 8
 US-10-632-150-2
 ; Sequence 2, Application US/10632150
 ; Publication No. US2005025187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chiaux, D.
 ; APPLICANT: Pagano, M.
 ; APPLICANT: Latres, E.
 ; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
 ; FILE REFERENCE: 5914-081
 ; CURRENT APPLICATION NUMBER: US/10/632,150
 ; CURRENT FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: US/09/385,219
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: 60/098,355
 ; PRIOR FILING DATE: 1998-08-28
 ; PRIOR APPLICATION NUMBER: 60/118,568
 ; PRIOR FILING DATE: 1999-02-03
 ; PRIOR APPLICATION NUMBER: 60/124,449
 ; PRIOR FILING DATE: 1999-03-15
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-632-150-2

Query Match 82.8%; Score 2384.5; DB 5; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 QY 1 MDP-DSVIEDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 DB 1 MDPAAVLQEKALKFMNNSEREDCNGEPKRIIPEKNSLRQTYNSCARLCLNQETVCLA 60
 QY 37 SCLQSPSVRCI--OISNGTSSVIVSRKPSBGNVQKEKDLCKIKYFDOWSESQVEFVE 93
 DB 61 S--TAMKTENCVAKTKLANGTSMIVPKORKLSASYEKEKELCVKTFEOWSESQVEFVE 118
 QY 94 HLISRMCHYQHGHSINLYKPMQLQDFITALPEQGLDHAENILSYLDARSCLAAELVCKE 153
 DB 119 HLISQWCHYQHGHSINLYKPMQLQDFITALPARGLDHAENILSYLDARSCLAAELVCKE 178
 QY 154 WQVISEGMLWKKLIEMVVRTDPLWKLGERGWDQYLFKNRPTDG--PPNSFYRSLYK 211
 DB 179 WYRVTSQGLWKKLIEMVVRTDSLWGLAERRGWQYLFKNRPPDGNAPPNSFYRSLYK 238
 QY 212 IIODIETIESNRCGRHNLQRCSENSKGVYCLQYDDDEKILISGLRDNISIKWDKTSLE 271
 DB 239 IIODIETIESNRCGRHNLQRCSENSKGVYCLQYDDQKIVSGURDNITIKWDKNTLE 298
 QY 272 CLKVLGTGHTGSLVCLQYDERVITGSSDSTVRVWDVNTGEVNTLIHNEAVLHLRFSNG 331
 DB 299 CKRILGTGHTGSLVCLQYDERVITGSSDSTVRVWDVNTGEVNTLIHNEAVLHLRFSNG 358
 QY 332 LMVTCCKRSIAVMDMASATDITLRLVVGHRAAVNVVDFDDKIIVSASGDRTIKWNSTS 391
 DB 359 MMVTCCKRSIAVMDMASPTDITLRLVVGHRAAVNVVDFDDKIIVSASGDRTIKWNSTS 418
 QY 392 TCEVFTLNGHKGACIACQYRDLRVVSGSSDNTIRLWDIECGACIACLRVLGHEELVRCIRF 451
 DB 419 TCEVFTLNGHKGACIACQYRDLRVVSGSSDNTIRLWDIECGACIACLRVLGHEELVRCIRF 478
 QY 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRITLVHSGRVRFLQDFEQIISSSH 511

QY 392 TCEVFTLNGHKGACIACQYRDLRVVSGSSDNTIRLWDIECGACIACLRVLGHEELVRCIRF 451
 DB 419 TCEVFTLNGHKGACIACQYRDLRVVSGSSDNTIRLWDIECGACIACLRVLGHEELVRCIRF 478
 QY 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRITLVHSGRVRFLQDFEQIISSSH 511
 DB 479 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRITLVHSGRVRFLQDFEQIISSSH 538
 QY 512 DTILWDFLNVPPSAQNETRSPSRITYISR 542
 DB 539 DTILWDFLNDPAQAEPSPSRITYISR 569

RESULT 9
 US-11-073-485-2
 ; Sequence 2, Application US/11073485
 ; Publication No. US20050208601A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, M.
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
 ; FILE REFERENCE: 5914-090-999
 ; CURRENT APPLICATION NUMBER: US/11/073,485
 ; CURRENT FILING DATE: 2005-03-04
 ; PRIOR APPLICATION NUMBER: 10/042,417
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 60/260,179
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-073-485-2

Query Match 82.8%; Score 2384.5; DB 6; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 QY 1 MDP-DSVIEDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 DB 1 MDPAAVLQEKALKFMNNSEREDCNGEPKRIIPEKNSLRQTYNSCARLCLNQETVCLA 60
 QY 37 SCLQSPSVRCI--OISNGTSSVIVSRKPSBGNVQKEKDLCKIKYFDOWSESQVEFVE 93
 DB 61 S--TAMKTENCVAKTKLANGTSMIVPKORKLSASYEKEKELCVKTFEOWSESQVEFVE 118
 QY 94 HLISRMCHYQHGHSINLYKPMQLQDFITALPEQGLDHAENILSYLDARSCLAAELVCKE 153
 DB 119 HLISQWCHYQHGHSINLYKPMQLQDFITALPARGLDHAENILSYLDARSCLAAELVCKE 178
 QY 154 WQVISEGMLWKKLIEMVVRTDPLWKLGERGWDQYLFKNRPTDG--PPNSFYRSLYK 211
 DB 179 WYRVTSQGLWKKLIEMVVRTDSLWGLAERRGWQYLFKNRPPDGNAPPNSFYRSLYK 238
 QY 212 IIODIETIESNRCGRHNLQRCSENSKGVYCLQYDDDEKILISGLRDNISIKWDKTSLE 271
 DB 239 IIODIETIESNRCGRHNLQRCSENSKGVYCLQYDDQKIVSGURDNITIKWDKNTLE 298
 QY 272 CLKVLGTGHTGSLVCLQYDERVITGSSDSTVRVWDVNTGEVNTLIHNEAVLHLRFSNG 331
 DB 299 CKRILGTGHTGSLVCLQYDERVITGSSDSTVRVWDVNTGEVNTLIHNEAVLHLRFSNG 358
 QY 332 LMVTCCKRSIAVMDMASATDITLRLVVGHRAAVNVVDFDDKIIVSASGDRTIKWNSTS 391
 DB 359 MMVTCCKRSIAVMDMASPTDITLRLVVGHRAAVNVVDFDDKIIVSASGDRTIKWNSTS 418
 QY 392 TCEVFTLNGHKGACIACQYRDLRVVSGSSDNTIRLWDIECGACIACLRVLGHEELVRCIRF 451
 DB 419 TCEVFTLNGHKGACIACQYRDLRVVSGSSDNTIRLWDIECGACIACLRVLGHEELVRCIRF 478
 QY 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRITLVHSGRVRFLQDFEQIISSSH 511

/ Sequence 12, Application US/11099691
/ Publication No. US20050260644A1
/ GENERAL INFORMATION:
/ APPLICANT: INCYTE PHARMACEUTICALS, INC.
/ APPLICANT: BANDMAN, Olga
/ APPLICANT: HILLMAN, Jennifer L.
/ APPLICANT: LAL, Preeti
/ APPLICANT: YUE, Henry
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: PATTERSON, Chandra
/ APPLICANT: BAUGHN, Mariah R.
/ APPLICANT: YANG, Junming
/ TITLE OF INVENTION: CELL SIGNALING PROTEINS
/ FILE REFERENCE: PF-0521 PCT
/ CURRENT APPLICATION NUMBER: US/11/099,691
/ CURRENT FILING DATE: 2005-04-06
/ PRIOR APPLICATION NUMBER: US/09/700,444
/ PRIOR FILING DATE: 2002-08-26
/ PRIOR APPLICATION NUMBER: 60/085,343
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/098,010
/ PRIOR FILING DATE: 1998-08-26
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PERL Program
/ SEQ ID NO 12
/ LENGTH: 569
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc-feature
/ OTHER INFORMATION: Incyte Clone 3239149
US-11-099-691-12

Query Match 82.8%; Score 2384.5; DB 6; Length 569;
Best Local Similarity 79.0%; Pred. No. 5.3e-201;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
DB 1 MPAEAVLQEKALKFNNSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNQEVVCLA 60
QY 37 SCLQSMPSVRCL---QISNGTSSVIVSRKRPSEGNKYQEKDLCIKYFDQWSESQDQVEFVE 93
DB 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKELCVKVFQWSESQDQVEFVE 118
QY 94 HLISRMCHYQHGHINSYLPKMLQDFITALPQGLDHIHAENILSYLDARSLCAAEVLVCKE 153
DB 119 HLISQWCHYQHGHINSYLPKMLQDFITALPARGLDHIAENILSYLDAKSLCAAEVLVCKE 178
QY 154 WORVISEGMLWKKLIERMVRTDPLWGLSERGWDQYLFKNRPTDG--PPNSFYRSLYPK 211
DB 179 WYRVTS DGMWKKLIERMVRTDPLWGLSERGWDQYLFKNRPPDGNAPPNSFYRALYPK 238
QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDDEKIIISGLRDNISIKIWDKTSLE 271
DB 239 IIQDIETIESNRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 298
QY 272 CLKVLGTGHTGSLVCLQYDQVITGSSDSTVRVWVNTGEVLTNLIHNEAVLHLRFSNG 331
DB 299 CKRILGTGHTGSLVCLQYDQVITGSSDSTVRVWVNTGEVLTNLIHNEAVLHLRFSNG 358
QY 332 LMVTCCKDRSIAVMDWASATDITLRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWNTS 391
DB 359 MMVTCCKDRSIAVMDWASPTDITLRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWNTS 418
QY 392 TCFEVRTLNGHKGKGIACQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 451
DB 419 TCFEVRTLNGHKGKGIACQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTLVEHSGRVFRLQDFEQIISSSH 511
DB 479 DNKRIVSGAYDGKIKVMDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQDFEQIISSSH 538

QY 512 DTILWDFLNVPPSAQNETRSPSRVTYYSR 542
DB 539 DTILWDFLNDPAAQAEPSPSRVTYYSR 569
RESULT 13
US-11-073-460-2
/ Sequence 2, Application US/11073460
/ Publication No. US20050272066A1
/ GENERAL INFORMATION:
/ APPLICANT: Pagano, M.
/ TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
/ TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
/ FILE REFERENCE: 5914-090-999
/ CURRENT APPLICATION NUMBER: US/11/073,460
/ CURRENT FILING DATE: 2005-03-04
/ PRIOR APPLICATION NUMBER: 10/042,417
/ PRIOR FILING DATE: 2002-01-07
/ PRIOR APPLICATION NUMBER: 60/260,179
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 569
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-073-460-2
Query Match 82.8%; Score 2384.5; DB 6; Length 569;
Best Local Similarity 79.0%; Pred. No. 5.3e-201;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
DB 1 MPAEAVLQEKALKFNNSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNQEVVCLA 60
QY 37 SCLQSMPSVRCL---QISNGTSSVIVSRKRPSEGNKYQEKDLCIKYFDQWSESQDQVEFVE 93
DB 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKELCVKVFQWSESQDQVEFVE 118
QY 94 HLISRMCHYQHGHINSYLPKMLQDFITALPQGLDHIHAENILSYLDARSLCAAEVLVCKE 153
DB 119 HLISQWCHYQHGHINSYLPKMLQDFITALPARGLDHIAENILSYLDAKSLCAAEVLVCKE 178
QY 154 WORVISEGMLWKKLIERMVRTDPLWGLSERGWDQYLFKNRPTDG--PPNSFYRSLYPK 211
DB 179 WYRVTS DGMWKKLIERMVRTDPLWGLSERGWDQYLFKNRPPDGNAPPNSFYRALYPK 238
QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDDEKIIISGLRDNISIKIWDKTSLE 271
DB 239 IIQDIETIESNRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 298
QY 272 CLKVLGTGHTGSLVCLQYDQVITGSSDSTVRVWVNTGEVLTNLIHNEAVLHLRFSNG 331
DB 299 CKRILGTGHTGSLVCLQYDQVITGSSDSTVRVWVNTGEVLTNLIHNEAVLHLRFSNG 358
QY 332 LMVTCCKDRSIAVMDWASATDITLRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWNTS 391
DB 359 MMVTCCKDRSIAVMDWASPTDITLRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWNTS 418
QY 392 TCFEVRTLNGHKGKGIACQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 451
DB 419 TCFEVRTLNGHKGKGIACQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTLVEHSGRVFRLQDFEQIISSSH 511
DB 479 DNKRIVSGAYDGKIKVMDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQDFEQIISSSH 538
QY 512 DTILWDFLNVPPSAQNETRSPSRVTYYSR 542
DB 539 DTILWDFLNDPAAQAEPSPSRVTYYSR 569

RESULT 14
US-10-687-732-18
; Sequence 18, Application US/10687732
; Publication No. US20040171074A1
; GENERAL INFORMATION:
; APPLICANT: Orlicky, Stephen
; APPLICANT: Sicherl, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; APPLICANT: Tang, Xiaojing
; TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
; FILE REFERENCE: 14096.34USU1
; CURRENT APPLICATION NUMBER: US/10/687,732
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,606
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank/NP_033901
; DATABASE ENTRY DATE: 1998-08-04
; RELEVANT RESIDUES: (1)..(569)
US-10-687-732-18

Query Match 82.5%; Score 2375.5; DB 4; Length 569;
Best Local Similarity 78.6%; Pred. No. 3.3e-200;
Matches 449; Conservative 49; Mismatches 42; Indels 31; Gaps 7;
QY 1 MDP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
Db 1 MDPAAVLQERKALFMSNREDCCNNGEPKRIPEKNSLRQTYNSCARLINCQETVCLT 60
QY 37 SCLQMPVSRLC---QISNGTSSVIVSRKRSEGNVQKEKLCIKYFQWSESQVEVE 93
Db 61 S--TAMKTCNCVAKLANGTSSMIVPKRKLASAYEKEKLCVKYFQWSESQVEVE 118
QY 94 HLISWCHYOHGHINSYKLPMLQRFITALPQGHLDHIAENILSYLDARSLCAAEVLCKE 153
Db 119 HLISQCHYOHGHINSYKLPMLQRFITALPARGLDHIAENILSYLDARSLCAAEVLCKE 178
QY 154 MQRVISEGMLWKLLIERMVRTDPLWKLSERRGWDQYLFKNRPTD--GPPNSFYRSLYK 211
Db 179 WYRVTSQGLWKLIERMVRTDPLWKLSERRGWDQYLFKNRPTD--GPPNSFYRSLYK 238
QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRDNSTKIWDKSTLE 271
Db 239 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRDNSTKIWDKSTLE 298
QY 272 CLKVLGTGTSVLCQYDERVITVGTSSDSTVRVWVNTGEVNTLIHNEAVLHLRFNSG 331
Db 299 CKRILTGTGTSVLCQYDERVITVGTSSDSTVRVWVNTGEVNTLIHNEAVLHLRFNSG 358
QY 332 LMVTCCKRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMWTS 391
Db 359 MMTVTCCKRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMWTS 418
QY 392 TCFVRTLNGHKGRIACIQYORLRLVVGSSDNTIRLWDLIECGACLRVLGHEELVRCIRF 451
Db 419 TCFVRTLNGHKGRIACIQYORLRLVVGSSDNTIRLWDLIECGACLRVLGHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKI KVMWDLQAALDPRAPATLCLRTLVEHSGRVFRLQDFEQIISSHD 511
Db 479 DNKRIVSGAYDGKI KVMWDLQAALDPRAPATLCLRTLVEHSGRVFRLQDFEQIISSHD 538
QY 512 DTILWDLNVPVPSAQNETRSPRTYTIYSR 542
Db 539 DTILWDLNVPVPSAQNETRSPRTYTIYSR 569

RESULT 15
US-11-097-143-6363
; Sequence 6363, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6363
; LENGTH: 510
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-6363

Query Match 72.2%; Score 2077.5; DB 6; Length 510;
Best Local Similarity 80.8%; Pred. No. 5.2e-174;
Matches 384; Conservative 44; Mismatches 46; Indels 1; Gaps 1;
QY 61 RKRSEGNVQKEKLCIKYFQWSESQVEVEHLISRMCHYQHGHINSYKLPMLQRFI 120
Db 30 RKRSEGNVQKEKLCIKYFQWSESQVEVEHLISRMCHYQHGHINSYKLPMLQRFI 89
QY 121 TALPEQGLDHTAENILSYLDARSLCAAEVLCKEQRVISEGMLWKLLIERMVRTDPLWKG 180
Db 90 TLLPTKGLDHTAENILSYLDARSLCAAEVLCKEQRVISEGMLWKLLIERMVRTDPLWKG 149
QY 181 LSERRGWDQYLFKNRPTDGP--PNSFYRSLYKPIIOTDIETIESNRCGRHNLQRIQCRSEN 239
Db 150 LAERNMNVYLFKPRPGQTQPHSPHRELFPKIMNDISIEENNMTGRHMLRRINCRSEN 209
QY 240 SKGVYCLQYDDEKIIISGLRDNSTKIWDKTSLECLKVLGTGTSVLCQYDDEKIIISGSD 299
Db 210 SKGVYCLQYDDEKIIISGLRDNSTKIWDKTSLECLKVLGTGTSVLCQYDDEKIIISGSD 269
QY 300 STVRVWVNTGEVNTLIHNEAVLHLRFNSGLMVTCSKDRSIAVWDMASATDITLRRVL 359
Db 270 STVRVWVNTGEVNTLIHNEAVLHLRFNSGLMVTCSKDRSIAVWDMASATDITLRRVL 329
QY 360 VGHRAAVNVVDFDKYIVSASGDRTIKVMWTSSTCFEVRTLNGHKGRIACIQYORLRLVVG 419
Db 330 VGHRAAVNVVDFDKYIVSASGDRTIKVMWTSSTCFEVRTLNGHKGRIACIQYORLRLVVG 389
QY 420 SSDNTIRLWDLIECGACLRVLGHEELVRCIRFDTKRIVSGAYDGKI KVMWDLQAALDPRAP 479
Db 390 SSDNTIRLWDLIECGACLRVLGHEELVRCIRFDTKRIVSGAYDGKI KVMWDLQAALDPRAP 449
QY 480 ASTLCRLTLVEHSGRVFRLQDFEQIISSHDDTILWDLNVPVPSAQNETRSPS 534
Db 450 SNTLCRLTLVEHSGRVFRLQDFEQIISSHDDTILWDLNVPVPSAQNETRSPS 504

Search completed: August 25, 2006, 07:38:23
Job time : 187 secs

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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:35:27 ; Search time 34 Seconds
(without alignments)
1090.736 Million cell updates/sec

Title: US-10-665-715-16

Perfect score: 2879

Sequence: 1 MEPDSVIEDKTIELMCSVPR.....PPSAQNETRSPRTYISR 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2879	100.0	542	US-10-968-871-6	Sequence 6, Appli
2	2384.5	82.8	569	US-10-968-871-3	Sequence 3, Appli
3	2384.5	82.8	569	US-11-106-014-2	Sequence 2, Appli
4	416.5	14.5	1281	US-10-449-902-42332	Sequence 42332, A
5	395	13.7	415	US-11-293-697-4324	Sequence 4324, Ap
6	329.5	11.4	317	US-11-056-3558-90488	Sequence 90488, A
7	329.5	11.4	317	US-11-056-3558-94244	Sequence 94244, A
8	327.5	11.4	422	US-11-106-014-4	Sequence 4, Appli
9	326	11.3	891	US-10-449-902-54504	Sequence 54504, A
10	323	11.2	267	US-11-056-3558-37531	Sequence 37531, A
11	323	11.2	267	US-11-056-3558-85524	Sequence 85524, A
12	323	11.2	333	US-11-056-3558-37530	Sequence 37530, A
13	323	11.2	333	US-11-056-3558-85523	Sequence 85523, A
14	323	11.2	654	US-10-449-902-50780	Sequence 50780, A
15	318.5	11.1	808	US-10-449-902-41350	Sequence 41350, A
16	308.5	10.7	319	US-11-056-3558-13097	Sequence 13097, A
17	308.5	10.7	346	US-11-056-3558-13096	Sequence 13096, A
18	292.5	10.2	1194	US-11-045-540-2	Sequence 2, Appli
19	292.5	10.2	1205	US-11-045-540-3	Sequence 3, Appli
20	289	10.0	324	US-10-449-902-36608	Sequence 36608, A
21	286.5	10.0	326	US-11-056-3558-26606	Sequence 26606, A
22	286.5	10.0	326	US-11-056-3558-38851	Sequence 38851, A
23	286.5	10.0	326	US-11-056-3558-86112	Sequence 86112, A
24	284.5	9.9	326	US-11-056-3558-24773	Sequence 24773, A
25	283.5	9.8	311	US-10-953-349-37148	Sequence 37148, A

ALIGNMENTS

RESULT 1

US-10-968-871-6

; Sequence 6, Application US/10968871

; Publication No. US20060177829A1

; GENERAL INFORMATION:

; APPLICANT: New York University

; APPLICANT: Pagano, Michele

; TITLE OF INVENTION: Methods to Identify Compounds Useful For Tumor Sensitization to

; TITLE OF INVENTION: DNA Damage

; FILE REFERENCE: 05986/0200145-US0

; CURRENT APPLICATION NUMBER: US/10/968,871

; CURRENT FILING DATE: 2004-10-18

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 542

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-968-871-6

Query Match 100.0%; Score 2879; DB 6; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.3e-224; Indels 0; Gaps 0;
Matches 542; Conservative 0; Mismatches 0;

QY	1	MEPDSVIEDKTIELMCSVPRSLWGCANLVESMCALSCLOSMPSVRCLOISNGTSSVIVS	60
DB	1	MEPDSVIEDKTIELMCSVPRSLWGCANLVESMCALSCLOSMPSVRCLOISNGTSSVIVS	60
QY	61	RKRSEGNVQKEKDCIKIFYDQWSSDQVEFVEHLISRMCHYQHGHINSYLKPMLODFI	120
DB	61	RKRSEGNVQKEKDCIKIFYDQWSSDQVEFVEHLISRMCHYQHGHINSYLKPMLODFI	120
QY	121	TALPEQGLDHTAENTLSYLDARSLCAAEVLCKEORVISEGMLWKKLIERMVTDPLWKG	180
DB	121	TALPEQGLDHTAENTLSYLDARSLCAAEVLCKEORVISEGMLWKKLIERMVTDPLWKG	180
QY	181	LSERGWGDOYLFKNRPTDGPNNFYSRLYPKIIQDIETTESNRCGRHNLQICRSSENS	240
DB	181	LSERGWGDOYLFKNRPTDGPNNFYSRLYPKIIQDIETTESNRCGRHNLQICRSSENS	240
QY	241	KGVCLOYDDEKIIISGLRDNSIKIWDKTSLECKVLGTGHTSVLCLOYDERVITGSSDS	300
DB	241	KGVCLOYDDEKIIISGLRDNSIKIWDKTSLECKVLGTGHTSVLCLOYDERVITGSSDS	300
QY	301	TVRVWDVNTGEVINTLIHHNEAVLHRSNGLMVTCSKDRSIADVMDASATDITLRRVLV	360
DB	301	TVRVWDVNTGEVINTLIHHNEAVLHRSNGLMVTCSKDRSIADVMDASATDITLRRVLV	360

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Qy 361 GHRAANVVDKXIVSASGRTIKWSTSTCEFVRTLNHGKGIACLOYRDLVSGS 420
Db 361 GHRAANVVDKXIVSASGRTIKWSTSTCEFVRTLNHGKGIACLOYRDLVSGS 420
Qy 421 SDNTRLWDIECGACLRVLGHEELVRCIRFDNKRIVSGAYDVGKIKWDLQAALDPAPA 480
Db 421 SDNTRLWDIECGACLRVLGHEELVRCIRFDNKRIVSGAYDVGKIKWDLQAALDPAPA 480
Qy 481 STLCLRTLVEHSGRFRLOQDFEQIISSHDDTLIWDFLNVPSPAQNTRSPSRTTYI 540
Db 481 STLCLRTLVEHSGRFRLOQDFEQIISSHDDTLIWDFLNVPSPAQNTRSPSRTTYI 540
Qy 541 SR 542
Db 541 SR 542

RESULT 2
US-10-968-871-3
; Sequence 3, Application US/10968871
; Publication No. US20060177829A1
; GENERAL INFORMATION:
; APPLICANT: New York University
; APPLICANT: Pagano, Michele
; TITLE OF INVENTION: Methods to Identify Compounds Useful For Tumor Sensitization to
; FILE REFERENCE: DNA Damage
; CURRENT APPLICATION NUMBER: US/10/968,871
; CURRENT FILING DATE: 2004-10-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-968-871-3

Query Match 82.8%; Score 2384.5; DB 6; Length 569;
Best Local Similarity 79.0%; Pred. No. 2e-184;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
Db 1 MDPAEAVLQEKALKFPMNSEREDCNNGEPKRIIPEKNSLRQTYNSCARCLNQETVCLA 60
Qy 37 SCLOSMPSVRCL---QISNGTSSVIVSRKRPSEGNQYQEKDLCIKYFDQWSESQDVEFVE 93
Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYFEQWSESQDVEFVE 118
Qy 94 HLISRMCHYQGHINSYLPKMLQDFITALPEQGLDHTAENILSYLDARSICAELVCKE 153
Db 119 HLISQMCHYQGHINSYLPKMLQDFITALPARGLDHIAENILSYLDAKSLCAELVCKE 178
Qy 154 WQVRISEGMKWKLIERWVRTDPLWGLSERRGWDQYLFKRPDTG--PPNSFYRSLYPK 211
Db 179 WYRVTSQGLMWKLIERWVRTDSLWRGLAERRGWQYLFKKNPPDGNAPPNSFYRSLYPK 238
Qy 212 IIQDIETIESNWRGCRHNLQIQCRESKSGVYCLQYDDDEKIIISGLRDNSTIKINDKTSLE 271
Db 239 IIQDIETIESNWRGCRHSIORHCRSETSKGVYCLQYDDQKIVSGLRDNTIKINDKNTLE 298
Qy 272 CLKVLTGHTGSLVLCQYDERVITGSSDSTVRVWDVNTGEVLTNLIHNEAVLHLRFNSG 331
Db 299 CKRILTGHTGSLVLCQYDERVITGSSDSTVRVWDVNTGEVLTNLIHNEAVLHLRFNSG 358
Qy 332 LMVTCSDRSSTAVWDMASPTDITLRRVLVGHRAAANNVVDQDKYIVSASGRTIKVWSTS 391
Db 359 NMVTCSDRSSTAVWDMASPTDITLRRVLVGHRAAANNVVDQDKYIVSASGRTIKVWNIS 418
Qy 392 TCEFVRTLNHGKGIACLOYRDLVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 451
Db 419 TCEFVRTLNHGKGIACLOYRDLVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
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Qy 452 DNKRIVSGAYDGKIKWDLQAALDPAPASTLCLRTLVEHSGRFRLOQDFEQIISSHD 511
Db 479 DNKRIVSGAYDGKIKWDLVAALDPAPAGTLCRLTLVEHSGRFRLOQDFEQIIVSSHD 538
Qy 512 DTILIMDFLNVPSPAQNTRSPSRTTYISR 542
Db 539 DTILIMDFLNPAQAEPSPSRTTYISR 569

RESULT 3
US-11-106-014-2
; Sequence 2, Application US/11106014
; Publication No. US20060088846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiaux, Dah Sharim
; APPLICANT: Latres, Esther
; APPLICANT: Srivastava, Promod
; APPLICANT: Chandawarker, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; FILE REFERENCE: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; CURRENT APPLICATION NUMBER: US/11/106,014
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-2

Query Match 82.8%; Score 2384.5; DB 7; Length 569;
Best Local Similarity 79.0%; Pred. No. 2e-184;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
Db 1 MDPAEAVLQEKALKFPMNSEREDCNNGEPKRIIPEKNSLRQTYNSCARCLNQETVCLA 60
Qy 37 SCLOSMPSVRCL---QISNGTSSVIVSRKRPSEGNQYQEKDLCIKYFDQWSESQDVEFVE 93
Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYFEQWSESQDVEFVE 118
Qy 94 HLISRMCHYQGHINSYLPKMLQDFITALPEQGLDHTAENILSYLDARSICAELVCKE 153
Db 119 HLISQMCHYQGHINSYLPKMLQDFITALPARGLDHIAENILSYLDAKSLCAELVCKE 178
Qy 154 WQVRISEGMKWKLIERWVRTDPLWGLSERRGWDQYLFKRPDTG--PPNSFYRSLYPK 211
Db 179 WYRVTSQGLMWKLIERWVRTDSLWRGLAERRGWQYLFKKNPPDGNAPPNSFYRSLYPK 238
Qy 212 IIQDIETIESNWRGCRHNLQIQCRESKSGVYCLQYDDDEKIIISGLRDNSTIKINDKTSLE 271
Db 239 IIQDIETIESNWRGCRHSIORHCRSETSKGVYCLQYDDQKIVSGLRDNTIKINDKNTLE 298
Qy 272 CLKVLTGHTGSLVLCQYDERVITGSSDSTVRVWDVNTGEVLTNLIHNEAVLHLRFNSG 331
Db 299 CKRILTGHTGSLVLCQYDERVITGSSDSTVRVWDVNTGEVLTNLIHNEAVLHLRFNSG 358
Qy 332 LMVTCSDRSSTAVWDMASPTDITLRRVLVGHRAAANNVVDQDKYIVSASGRTIKVWSTS 391
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; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4324
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4324

Query Match      13.7%; Score 395; DB 7; Length 415;
Best Local Similarity 25.8%; Pred. No. 4.5e-24;
Matches 103; Conservative 79; Mismatches 140; Indels 78; Gaps 15;

Db 359 MMTVCSKORSIAVMDMASPTDITLRVLVGHRAAVNVVDFDKYIVSASGDRITIKVNTS 418
Qy 392 TCFVRLTLNGKRGIACTQYRLRVVSSGSDNTIRLWDIECCACILRVLEGHEELVRCIRF 451
Db 419 TCFVRLTLNGKRGIACTQYRLRVVSSGSDNTIRLWDIECCACILRVLEGHEELVRCIRF 478
Qy 452 DNKRIVSGAYDGKIKVMDLQALDPRAPASTLCRLTLVEHSGRVFRLQDFEQIISSHD 511
Db 479 DNKRIVSGAYDGKIKVMDLQALDPRAPAGTLCRLTLVEHSGRVFRLQDFEQIISSHD 538
Qy 512 DTILWDFLNVPSAQNETRSPSRITYTISR 542
Db 539 DTILWDFLNDPAQAEPSPSRITYTISR 569

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RESULT 4
US-10-449-902-42332
; Sequence 42332, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-393870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 42332
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-42332

Query Match      14.5%; Score 416.5; DB 6; Length 1281;
Best Local Similarity 35.8%; Pred. No. 3.8e-25;
Matches 105; Conservative 49; Mismatches 104; Indels 35; Gaps 9;

Db 249 DEKIISGLRDSIKIWDKTSLECKVLGTGHSV--LCLQYDERVIVTGSSDSTVRVWD 306
Qy 746 DGQVVSGSYDQTLRWDAATGECVRELQHTSLFVAVALSADGQIRVSGSGLTLARVWD 805
Db 307 VNTGEVLNLIHNEAVLHRLSNG--LMVTCCKORSIAVMDMASATDITLRLVGHRA 364
Qy 806 TATGETLRELKGTGWRSVAFSTDGQIRVITGGDQSVRVWDASTGECV---RELKGYTA 862
Db 365 AVNVVDF--DDKYIVSASGDRITIKVMTSTCFVRLTNGHKGIACTQYR--DRLVWSSG 420
Qy 863 ALISVAFSPDQIRIVSGGDDQTVRVNNAATGECQCEKLGHTQVDSIAFSPDQIHVSGS 922
Db 421 SNTIRLWDIEC-----GACLRVLEGHEELVRCIRF--DNKRIVSGAYDGKIKV 467
Qy 923 IDQTLRVMDVSSLSLSPSSSSGGAGLRERQGHTRKDVNSVAFPPDGKRLASGSDQSVRV 982
Db 468 WDLQALDPRAPASTLCRLTLVEHSGRVFRLQF--DEFQIISSHDDTILWID 518
Qy 983 WD-----AVSGELLHELQHGSGWRCVRFSPDQIRVSGSDDTQVRLWD 1026

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RESULT 5
US-11-293-697-4324
; Sequence 4324, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdna

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; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4324
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4324

Query Match      13.7%; Score 395; DB 7; Length 415;
Best Local Similarity 25.8%; Pred. No. 4.5e-24;
Matches 103; Conservative 79; Mismatches 140; Indels 78; Gaps 15;

Qy 167 LIERMVRTDPLW-----KGLSERGMDO-----YLPK-----NRPDGP 200
Db 44 LVEEIQKAEPLLTASRTQVKLLIQRLQELQKQNSHTFYLPKVLKAHILPLTNVALNKS 103
Qy 201 PNSFVRSLYPKII-----QDIETIESNWRGHRNLQIQRSENSKGVYCLQYDD-- 250
Db 104 GSCFTIGSYDRYCKLWDTASGEELNLE-----GHRNV-----VTAIAFNPPY 146
Qy 251 -EKIISGLRDSIKIWDKTSLECKVLGTGHSVLCLOYDER--VIVTGSSDSTVRVWDV 307
Db 147 GDKATGSGFDKTKLMSVETGCKYHTFRGHTAEIVCLSFNQSTLAVTGSMDDTTAKLWDI 206
Qy 308 NTGEVLNLIHNEAVLHRLF--SNGLMVTCCKORSIAVMDMASATDITLRLVGHRAA 365
Db 207 QNGEVTYLRGHSABEIIISLFSNTSGDRIITGTFDHTVVVWDADTGRKV---NILHCAE 263
Qy 366 VNVVDF--DDKYIVSASGDRITIKVMTSTCFVRLTNGHKGRI--ACQYRDLRVVSGSS 421
Db 264 ISSASFNWDCSLILITGSMDKTKLWDATNGKCVATLTGHDDDEILDSCFDYTKGLIATASA 323
Qy 422 DNTIRLWDIECGACLRVLEGHEELVRCIRFD--NKRIVSGAYDGKIKVMDLQALDPRAP 479
Db 324 DGTARIFSAATRKCLAKLEGHEGEISKISFNPQGNHLLTGSSDKTARIWDAQTG----- 377
Qy 480 ASTLCRLTLVHSGRVFRLQDFEQ--IISSHDDTILWID 517
Db 378 ---OCLQVLEGHTDEIFSCAFNYKGNIVITGSKONTCRIW 414

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RESULT 6
US-11-056-355B-90488
; Sequence 90488, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 90488
; LENGTH: 317
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(317)
; OTHER INFORMATION: Ceres Seq. ID no. 12724103
US-11-056-355B-90488

Query Match      11.4%; Score 329.5; DB 7; Length 317;
Best Local Similarity 31.0%; Pred. No. 6.1e-19;

```

Matches	76;	Conservative	50;	Mismatches	102;	Indels	17;	Gaps	7;
Qy	238	ENSGKVYCLQYDDKEKIIISGLRDNISIKIWDKTSLECLKVLTGHTGSVLCLOYD--ERVIVT	295						
Db	71	ENGISDVAFSSDARFIVSASDDKTLKLDVETGSLIKTLIGHTNYAFVCFNFPQSNMIVS	130						
Qy	296	GSSDSTVRVVDVNTGEVLTLLIHNEAVLHLRFS--NGLMVCYSKDRSIAVDMASATDI	353						
Db	131	GSPDETVRIMDVTTGCKLVLPADSDPVTADEFNRDGLSVSSSYDGLCRIWD--SGTGH	188						
Qy	354	TLRRVLVGHRAAVNVVDF--DDKIVISASGDRTIKWMTSTCFEVRTLNGHKGRIACLQ-	410						
Db	189	CVKTLIDENPPVSFVAFSPNGKFILVCTLDNTLRLWNISSAKFLKTYTGHVNAQYCISS	248						
Qy	411	----YRDLVYVSGSDNTIRLWDIECGACLRVLESGHEEL--VRCIRFDNKRIVYSGAVDG	463						
Db	249	AFSVYTGKRIYVSGSEDNCVHWMELNSKKLQKLGHTETVNVNACHPTEN-LIASGSLDK	307						
Qy	464	KIKW 468							
Db	308	TVRIW 312							

```

RESULT 7
US-11-056-355B-94244
; Sequence 94244, Application US/11056355B
; Publication NO. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 94244
; LENGTH: 317
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(317)
; OTHER INFORMATION: Ceres Seq. ID no. 12724103
US-11-056-355B-94244

```

Query Match	11.4%	Score 329.5;	DB 7;	Length 317;
Best Local Similarity	31.0%;	Pred. No. 6.le-19;		
Matches	76;	Conservative 50;	Mismatches 102;	Indels 17; Gaps 7;
Qy	238	ENSGGVYCLQYDDEKIIISGLRDNSTKIWDKTSLECLKVLGTGHTGSVLCLOYD--ERVIVT	295	
Db	71	ENGISDVAFFSDARFIVSASDDKTLKLDVETGSLIKTLIGHTNYAFVCNPNQSNMTIVS	130	
Qy	296	GSSDSTVRVWDVNTGEVLTNTLIHNEAVLHREFS--NGLMWTCSKDRSIAVWDMASATDI	353	
Db	131	GSFDETVRIVDVTGCKLVLPAAHSDPPTAVDFNRDGSLLIVSSVDGLCRWD--SGTGH	188	
Qy	354	TLRRVLVGHRAAVNVVDF--DDKYIVSASGORTIKVWSTSTCFEVRTLNGHKRGACIQ--	410	
Db	189	CVKTLIIDENPVPVFRSPNGCKFVLVGTLDNTLRLNMISSAKFLKTYTGHVNAQYCISS	248	
Qy	411	----YRDLRVGSGSDNTIRLWIDIECGACLRVLEGHEEL---VRCIRFDNKRIVSGAVDG	463	
Db	249	AFSVTNGKRIVSGSDNCVHWELNSKKLLQKLEGTETVMNVACHPTEN--LIASGSLDK	307	
Qy	464	KIKWV	468	
Db	308	TVRIW	312	

```

RESULT 8
US-11-106-014-4
; Sequence 4, Application US/11106014
; Publication No. US20060088846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiaur, Dah Sharim
; APPLICANT: Latres, Esther
; APPLICANT: Srivastava, Promod
; APPLICANT: Chandawarker, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106,014
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-4

Query Match      11.4%; Score 327.5; DB 7; Length 422;
Best Local Similarity 22.5%; Pred.No. 1.3e-18;
Matches 106; Conservative 77; Mismatches 137; Indels 151; Gaps 15;

QY      78 KYFDWSESDQVEF-----VHLLSRMCHYGHGHSYKPKMLORDFITALPEQ 126
DB      4 KDFETWLDNISVFLSLTDLOKNETDLHLISLSGAVQLRHLNNLETLKKRDFLKLPLE 63

QY      127 GLDHIAENILSYLDARSLCAELVCKEQRVVISGMLWKKLIERMVTDPLWKGLSERG 186
DB      64 ----LSFYLLKWLDPQTLLTCLVSKQWNKVIS-----ACTEYVWQTACKNLG 106

QY      187 WDQYLFKNRPTDGPNSF-YRSLYPKLIQDIETIESNWRGGRHNLQROCHSENSKSGYVC 245
DB      107 W-----QIDSDVDALHWKVKYKAILRKKQLEH-----136

QY      246 LOYDDEKIIISGLRDNISIKMDKTSLECLKVLVTGHTGSLVCLQYDERVIVTGSSTVRW 305
DB      137 -----EAFETSS-----LIGHSARVYALYKQGLLCTGSDLSAKLW 173

QY      306 DVNTGTEVLNTLIHNEAVLHLRFSNGLMVTCSKDRSAVWDMASATDITLRLVLGHRAA 365
DB      174 DVSTGQCVYGIQTH-----TCA-----190

QY      366 VNVYDFDDKYIVSAGDRTIKWMTSTCEVFRTLNGHKRGACIQYRDRL--VVVSGSDN 423
DB      191 --AVKFEQKLVGTSFNTVACWEMSSGARTQHFRGHTGAVFSVDYNDLDELIVSGSADF 248

QY      424 TIRLWDIECGACLRVLGHEE-----LVRC-----TRFDNKRIVSAGYDGKIKVWDLOA 472
DB      249 TVKWALSAGTCLNTLTAGHTEWTVKVLQCKVKSLLSHSPGDIYLLSADKYEIKWPIGR 308

QY      473 ALDPRAPASTLCRLTVEHSGRVF----RLQDFEQIISSHDDTILIWDF 519
DB      309 EINCK-----CLKTLVSVEDRSICLQRLHFDGKYIVCSSALG-LYQWDF 352

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US-10-449-902-54504
; Sequence 54504, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54504
; LENGTH: 891
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54504

Query Match      11.3%; Score 326; DB 6; Length 891;
Best Local Similarity 27.4%; Pred. No. 4.7e-18;
Matches 80; Conservative 61; Mismatches 119; Indels 32; Gaps 9;

QY 249 DDEKIISGLRDNISIKIWDKTSLECKVLTKHTGTSVLCL-----QYDERVIVTSSDSTVR 303
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 378 DEQYLAVATNLQVRVYDVASMSCSVLSGHTIEIVVCIDTICSSGKTLVVTGSKDSTVR 437

QY 304 VDVNTGVLNLTIIHNEAVLHLRF---SNGLMVTCSDKRSIAVW-----DMASATDI 353
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 438 LWMERRSCIGIGKGLGAIGSVAFSKSNKFNFSVSGSSDRTIKIWSDDTLDDVGSVEPL 497

QY 354 TLRRVLVGHRAAVN--VDFDDKIYVSASGDRTIKVMSTSTCEVFTLNGHKRGIACTQY 411
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 498 KAKAVAAHDKDINSLSVNDGLVCSGSEDTACIKLPLNLPVSVLKGHRGKLSWVEF 557

QY 412 R--DRLVVSGSSDNTIRLWDIECGACLRVLEHGLVRCIRF--DNKRIVSGAYDGKIRV 467
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 558 SPVEQCVITSSGDRTVKIVAWADGSLCTFEGHTSVLRSFSLSHGTQFVSCGSDGLVKL 617

QY 468 WDLQALADPRAPASTLCRLTLVEHSGRVPRLQF-DEFQIISSHDDTIL-IW 517
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 618 WTIK-----TNECIATFDKDKVWALAVGKKTEMLATGGTDAVLNLW 660

RESULT 10
US-11-056-355B-37531
; Sequence 37531, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 37531
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(267)
; OTHER INFORMATION: Ceres Seq. ID no. 12335591
US-11-056-355B-37531

Query Match      11.2%; Score 323; DB 7; Length 267;
Best Local Similarity 30.6%; Pred. No. 1.6e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

QY 223 WRCGRHNLQRCRSKNSKGVYCYQY--DDEKIISGLRDNISIKIWD-KTSLCKLVLTGH 279
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 4 WSATNYSL--IHRVEGSHSGISDLAWSSDSHYTCSASDDCTLRIDWARSFYECLEKVLRGH 61

QY 280 TGSVLCLOYD--ERVIVTSSDSTVRVWDVNTGEVLNLTIIHNEAV--LHLRFSNGLMVT 335
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 62 TNFVFCVNFNPPSNLIVSGSPDETIRIWEVTKGKVRMIKAHSMPISSVHFNRDGSLLVS 121

QY 336 CSKRSIAVWDMASATDITLRRVLVGHRAAVNVDF--DDKYIVSASGDRTIKVMSTSTC 393
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 122 ASHDGCKIWDKECT--CLKTLIDDKSPAVSFAKSPNGKFIIVATLDTLKLNYATG 179

QY 394 EIVRTLNHKGRIACLO-----YRDLVVSSSDNTIRLWDIECGACLRVLEHGBEL--- 445
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 180 KFLKVYTGHTNKFVTCITSAFVNTNGKIYVSGSDNCVYLWDLQARNILQRLLEGHTDAVIS 239

QY 446 VRCIRFDNKRIVSGAY-DGKIKVWDLOA 472
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 240 VSCHPVQNEISSGNHLDKTIIRWKQDA 267

RESULT 11
US-11-056-355B-85524
; Sequence 85524, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 85524
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(267)
; OTHER INFORMATION: Ceres Seq. ID no. 12680898
US-11-056-355B-85524

Query Match      11.2%; Score 323; DB 7; Length 267;
Best Local Similarity 30.6%; Pred. No. 1.6e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

QY 223 WRCGRHNLQRCRSKNSKGVYCYQY--DDEKIISGLRDNISIKIWD-KTSLCKLVLTGH 279
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 4 WSATNYSL--IHRVEGSHSGISDLAWSSDSHYTCSASDDCTLRIDWARSFYECLEKVLRGH 61

QY 280 TGSVLCLOYD--ERVIVTSSDSTVRVWDVNTGEVLNLTIIHNEAV--LHLRFSNGLMVT 335
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 62 TNFVFCVNFNPPSNLIVSGSPDETIRIWEVTKGKVRMIKAHSMPISSVHFNRDGSLLVS 121

QY 336 CSKRSIAVWDMASATDITLRRVLVGHRAAVNVDF--DDKYIVSASGDRTIKVMSTSTC 393
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 122 ASHDGCKIWDKECT--CLKTLIDDKSPAVSFAKSPNGKFIIVATLDTLKLNYATG 179

QY 394 EIVRTLNHKGRIACLO-----YRDLVVSSSDNTIRLWDIECGACLRVLEHGBEL--- 445
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 180 KFLKVYTGHTNKFVTCITSAFVNTNGKIYVSGSDNCVYLWDLQARNILQRLLEGHTDAVIS 239

QY 446 VRCIRFDNKRIVSGAY-DGKIKVWDLOA 472
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 240 VSCHPVQNEISSGNHLDKTIIRWKQDA 267

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Db 240 VSCHPVQNEISSGNHLDKTIIRWKQDA 267

RESULT 12
US-11-056-355B-37530
; Sequence 37530, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 37530
; LENGTH: 333
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(333)
; OTHER INFORMATION: Ceres Seq. ID no. 12335590
US-11-056-355B-37530

Query Match 11.2%; Score 323; DB 7; Length 333;
Best Local Similarity 30.6%; Pred. No. 2.2e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

Qy 223 WRCGRHNLRIQCRSENSKGVYCLQY--DDEKIISGLRDNISIKIWD-KTSLKLVLTGH 279
Db 70 WSATNYSL--IHRVEGHSSGISDLAWSSDSHYTCSASDDCTLRWDARSPEYCLKVLRGH 127
Qy 280 TGSVLCLOYD--ERVIVTSSDSTVRVWDVNTGEVLTNLHNEAV--LHLRFSNGLMVT 335
Db 128 TNFVFCVNFNPNSNLIVSGSFDETIIRWEVTKGKVRMIKAHSMPISSVHFNRDGLSIVS 187
Qy 336 CSKDRSIADVMDASATDITLRRVLVGHRAAVNVVDF--DDKYIVSASGDRITIKVWSTSTC 393
Db 188 ASHDSCKIWDKEGT--CLKTLIDDKSPAVSPAKFSPNGKFLIVATLDTSLKLSNYATG 245
Qy 394 EFVRTLNGHKRGIAQLQ-----YRDLRVSGSSDNTIRLWDIEGACLRVLEGHEEL--- 445
Db 246 KFLKVTYTGHTNKVFCITSAFVSVTNGKYIVSGSDNCVYLWDLQARNILQRLGHTDAVIS 305
Qy 446 VRCIRFDNKRIVSGAY-DGKIKVWDLOA 472
Db 306 VSCHPVQNEISSGNHLDKTIIRWKQDA 333

Query Match 11.2%; Score 323; DB 7; Length 333;
Best Local Similarity 30.6%; Pred. No. 2.2e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

Qy 223 WRCGRHNLRIQCRSENSKGVYCLQY--DDEKIISGLRDNISIKIWD-KTSLKLVLTGH 279
Db 70 WSATNYSL--IHRVEGHSSGISDLAWSSDSHYTCSASDDCTLRWDARSPEYCLKVLRGH 127
Qy 280 TGSVLCLOYD--ERVIVTSSDSTVRVWDVNTGEVLTNLHNEAV--LHLRFSNGLMVT 335
Db 128 TNFVFCVNFNPNSNLIVSGSFDETIIRWEVTKGKVRMIKAHSMPISSVHFNRDGLSIVS 187
Qy 336 CSKDRSIADVMDASATDITLRRVLVGHRAAVNVVDF--DDKYIVSASGDRITIKVWSTSTC 393
Db 188 ASHDSCKIWDKEGT--CLKTLIDDKSPAVSPAKFSPNGKFLIVATLDTSLKLSNYATG 245
Qy 394 EFVRTLNGHKRGIAQLQ-----YRDLRVSGSSDNTIRLWDIEGACLRVLEGHEEL--- 445
Db 246 KFLKVTYTGHTNKVFCITSAFVSVTNGKYIVSGSDNCVYLWDLQARNILQRLGHTDAVIS 305
Qy 446 VRCIRFDNKRIVSGAY-DGKIKVWDLOA 472
Db 306 VSCHPVQNEISSGNHLDKTIIRWKQDA 333

RESULT 13
US-11-056-355B-85523
; Sequence 85523, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 85523
; LENGTH: 333
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
```

```
; NAME/KEY: peptide
; LOCATION: (1)..(333)
; OTHER INFORMATION: Ceres Seq. ID no. 12680897
US-11-056-355B-85523

Query Match 11.2%; Score 323; DB 7; Length 333;
Best Local Similarity 30.6%; Pred. No. 2.2e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

Qy 223 WRCGRHNLRIQCRSENSKGVYCLQY--DDEKIISGLRDNISIKIWD-KTSLKLVLTGH 279
Db 70 WSATNYSL--IHRVEGHSSGISDLAWSSDSHYTCSASDDCTLRWDARSPEYCLKVLRGH 127
Qy 280 TGSVLCLOYD--ERVIVTSSDSTVRVWDVNTGEVLTNLHNEAV--LHLRFSNGLMVT 335
Db 128 TNFVFCVNFNPNSNLIVSGSFDETIIRWEVTKGKVRMIKAHSMPISSVHFNRDGLSIVS 187
Qy 336 CSKDRSIADVMDASATDITLRRVLVGHRAAVNVVDF--DDKYIVSASGDRITIKVWSTSTC 393
Db 188 ASHDSCKIWDKEGT--CLKTLIDDKSPAVSPAKFSPNGKFLIVATLDTSLKLSNYATG 245
Qy 394 EFVRTLNGHKRGIAQLQ-----YRDLRVSGSSDNTIRLWDIEGACLRVLEGHEEL--- 445
Db 246 KFLKVTYTGHTNKVFCITSAFVSVTNGKYIVSGSDNCVYLWDLQARNILQRLGHTDAVIS 305
Qy 446 VRCIRFDNKRIVSGAY-DGKIKVWDLOA 472
Db 306 VSCHPVQNEISSGNHLDKTIIRWKQDA 333

RESULT 14
US-10-449-902-50780
; Sequence 50780, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449.902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50780
; LENGTH: 654
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-50780

Query Match 11.2%; Score 323; DB 6; Length 654;
Best Local Similarity 25.9%; Pred. No. 5.4e-18;
Matches 86; Conservative 55; Mismatches 103; Indels 88; Gaps 12;

Qy 242 GVCY--LQYDDEKIISGLRDNISIKIWD-----KTS-----LE 271
Db 338 GLNCSSISHDGLSVVGGFSDSSVKVWDMKIGQPPKTSPPQGENGLSGERTSASDYKGR 397
Qy 272 CLKVLJTGHGTVLCLQYDE--RVIVTSSDSTVRVWDVNTGEVLTNLHNEAVLHLRFS 329
Db 398 PYTLFQHGSGPVYSAFSPFDFLLSSSDSTIRLW-----STKLNAN----- 440
Qy 330 NGLMVTCSKDRSIADVMDASATDITLRRVLVGHRAAVNVVDFDDDKYIVSASGDRITIKVWS 389
Db 441 ----LVCYKGNHVPVWDVQFSP-----VGH-----YFASASHDRTARIWS 476
Qy 390 TSTCEFVRTLNGHKRGIAQLQY--RDLRVSGSSDNTIRLWDIEGACLRVLEGHEELVR 447
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